

OM protein - protein search, using sw model

Run on: June 8, 2005, 12:16:33 ; Search time 124 Seconds
 (without alignments)
 368.046 Million cell updates/sec

Title: US-10-631-258-13
 Perfect score: 638
 Sequence: 1 VKLQESGPGGLVQPSQSL SIT.....SYPYNYFDVWGQGTTVTVSA 118

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

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 2: geneseqp1990s:*
 3: geneseqp2000s:*
 4: geneseqp2001s:*
 5: geneseqp2002s:*
 6: geneseqp2003as:*
 7: geneseqp2003bs:*
 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		Query				Description
No.	Score	Match	Length	DB	ID	
1	638	100.0	118	8	ADQ98036	Adq98036 Mutant mu
2	638	100.0	120	8	ADQ98119	Adq98119 Murine 2D
3	638	100.0	227	8	ADQ98061	Adq98061 Chimeric
4	638	100.0	254	8	ADQ98106	Adq98106 Chimeric
5	626	98.1	118	8	ADQ98034	Adq98034 Mutant mu
6	626	98.1	120	8	ADQ98117	Adq98117 Murine 2D
7	626	98.1	227	8	ADQ98059	Adq98059 Chimeric
8	626	98.1	254	8	ADQ98104	Adq98104 Chimeric
9	621	97.3	118	8	ADQ98033	Adq98033 Cloned hy

10	621	97.3	120	8	ADQ98116	Adq98116	Murine 2D
11	621	97.3	227	8	ADQ98058	Adq98058	Chimeric
12	621	97.3	227	8	ADQ98063	Adq98063	Chimeric
13	621	97.3	254	8	ADQ98103	Adq98103	Chimeric
14	621	97.3	254	8	ADQ98108	Adq98108	Chimeric
15	618	96.9	118	8	ADQ98109	Adq98109	Native hy
16	618	96.9	118	8	ADQ98064	Adq98064	Native hy
17	618	96.9	118	8	ADQ98032	Adq98032	Native hy
18	618	96.9	119	8	ADQ98028	Adq98028	Murine an
19	617	96.7	118	8	ADQ98035	Adq98035	Mutant mu
20	617	96.7	118	8	ADQ98037	Adq98037	Mutant mu
21	617	96.7	120	8	ADQ98120	Adq98120	Murine 2D
22	617	96.7	120	8	ADQ98118	Adq98118	Murine 2D
23	617	96.7	227	8	ADQ98062	Adq98062	Chimeric
24	617	96.7	227	8	ADQ98060	Adq98060	Chimeric
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26	617	96.7	254	8	ADQ98107	Adq98107	Chimeric
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32	498.5	78.1	492	8	ADQ91084	Adq91084	Antibody
33	498.5	78.1	492	8	ADQ91104	Adq91104	Antibody
34	498.5	78.1	492	8	ADQ91106	Adq91106	Antibody
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36	498.5	78.1	492	8	ADQ91086	Adq91086	Antibody
37	498.5	78.1	492	8	ADQ91092	Adq91092	Antibody
38	498.5	78.1	492	8	ADQ91094	Adq91094	Antibody
39	498.5	78.1	492	8	ADQ91100	Adq91100	Antibody
40	498.5	78.1	492	8	ADQ91096	Adq91096	Antibody
41	498.5	78.1	492	8	ADQ91098	Adq91098	Antibody
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43	498.5	78.1	492	8	ADQ91078	Adq91078	Bispecifi
44	497.5	78.0	450	3	AAY44991	Aay44991	M79scFv-i
45	497.5	78.0	451	8	ADR43339	Adr43339	scFv anti

ALIGNMENTS

RESULT 1

ADQ98036

ID ADQ98036 standard; protein; 118 AA.

XX

AC ADQ98036;

XX

DT 21-OCT-2004 (first entry)

XX

DE Mutant murine antibody 2D12.5 variable heavy chain protein N87D G54C.

XX

KW murine; mouse; mutant; mutein; antigen recognition domain;

KW in vivo imaging; cell-antibody-metal chelate complex;

KW emission tomography; magnetic resonance imaging; lanthanide luminescence;

KW gamma-emissions; single photon emission tomography; SPET; cancer;

KW cytostatic; immunosuppressive; multi-functional antibody; metal chelate.

XX

OS Mus musculus.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 54
FT /note= "Wild type Gly substituted for Cys"
FT Misc-difference 87
FT /note= "Wild type Asn substituted for Asp"
XX
PN WO2004065569-A2.
XX
PD 05-AUG-2004.
XX
PF 23-JAN-2004; 2004WO-US001808.
XX
PR 23-JAN-2003; 2003US-00350555.
PR 22-JUL-2003; 2003US-00625047.
PR 31-JUL-2003; 2003US-00631258.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Meares C, Corneillie T;
XX
DR WPI; 2004-580725/56.
DR N-PSDB; ADQ98042.
XX
PT Novel mutant antibody comprising reactive site not present in wild-type
PT of antibody and antigen recognition domain that recognizes macrocyclic
PT metal chelate having four nitrogen atoms, useful for treating cancer or
PT autoimmune diseases.
XX
PS Claim 41; SEQ ID NO 13; 208pp; English.
XX
CC This invention relates to multi-functional antibodies that recognise
CC chelating agents and metal chelates, particularly macrocyclic metal
CC chelates. Specifically, it refers to an antibody that comprises a metal
CC chelate bound to an antigen recognition domain, where the metal chelate
CC has a reactive functional group of complementary reactivity to the
CC reactive site of the antibody. This reactive site is the side chain of a
CC naturally occurring amino acid e.g. the -SH group side chain of a
CC cysteine residue (not present in the wild type) which can be used to form
CC a covalent bond between the reactive site of the antibody and the
CC reactive functional group of the metal chelate. The present invention
CC describes using these antibodies for in vivo imaging where the antibody
CC comprises a targeting moiety that binds specifically to a cell via a cell
CC surface receptor or antigen thus forming a cell-mutant antibody complex.
CC On addition of the metal chelate, a cell-antibody-metal chelate complex
CC is formed that can be detected using emission tomography, magnetic
CC resonance imaging, lanthanide luminescence, gamma-emissions or single
CC photon emission tomography (SPET). As such, this method is useful for
CC treating a subject with cancer and pharmaceutical compositions exhibit
CC cytostatic and immunosuppressive activities. This polypeptide sequence is
CC a mutant murine antibody 2D12.5 variable heavy chain protein of the
CC invention.
XX
SQ Sequence 118 AA;

Query Match 100.0%; Score 638; DB 8; Length 118;
Best Local Similarity 100.0%; Pred. No. 9.5e-55;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 VKLQESGPGLVQPSQSL SITCTVSGFSLTDYGVHWVRQSPGKGLEWLGVWSGCGTAYTA 60
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Db      1 VKLQESGPGLVQPSQSL SITCTVSGFSLTDYGVHWVRQSPGKGLEWLGVWSGCGTAYTA 60

Qy     61 AFISRLNIYKD NSKNQVFFEMNSLQADDTAMY YCARRGSYPYNYFDVWGQGT TVTVSA 118
          |||
Db     61 AFISRLNIYKD NSKNQVFFEMNSLQADDTAMY YCARRGSYPYNYFDVWGQGT TVTVSA 118
```

RESULT 2

ADQ98119

ID ADQ98119 standard; protein; 120 AA.

XX

AC ADQ98119;

XX

DT 21-OCT-2004 (first entry)

XX

DE Murine 2D12.5 antibody IgG1 heavy chain variable domain G55C N85D mutein.

XX

KW murine; mouse; magnetic resonance imaging; lanthanide luminescence;

KW gamma-emissions; single photon emission tomography; SPET; cancer;

KW cytostatic; immunosuppressive; multi-functional antibody; metal chelate;

KW antigen recognition domain; in vivo imaging;

KW cell-antibody-metal chelate complex; emission tomography; mutant; mutein.

XX

OS Mus musculus.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 55

FT /note= "Wild type Gly substituted for Cys"

FT Misc-difference 85

FT /note= "Wild type Asn substituted for Asp"

XX

PN WO2004065569-A2.

XX

PD 05-AUG-2004.

XX

PF 23-JAN-2004; 2004WO-US001808.

XX

PR 23-JAN-2003; 2003US-00350555.

PR 22-JUL-2003; 2003US-00625047.

PR 31-JUL-2003; 2003US-00631258.

XX

PA (REGC) UNIV CALIFORNIA.

XX

PI Meares C, Corneillie T;

XX

DR WPI; 2004-580725/56.

XX

PT Novel mutant antibody comprising reactive site not present in wild-type

PT of antibody and antigen recognition domain that recognizes macrocyclic

PT metal chelate having four nitrogen atoms, useful for treating cancer or

PT autoimmune diseases.

XX

PS Disclosure; SEQ ID NO 96; 208pp; English.

XX

CC This invention relates to multi-functional antibodies that recognise
 CC chelating agents and metal chelates, particularly macrocyclic metal
 CC chelates. Specifically, it refers to an antibody that comprises a metal
 CC chelate bound to an antigen recognition domain, where the metal chelate
 CC has a reactive functional group of complementary reactivity to the
 CC reactive site of the antibody. This reactive site is the side chain of a
 CC naturally occurring amino acid e.g. the -SH group side chain of a
 CC cysteine residue (not present in the wild type) which can be used to form
 CC a covalent bond between the reactive site of the antibody and the
 CC reactive functional group of the metal chelate. The present invention
 CC describes using these antibodies for in vivo imaging where the antibody
 CC comprises a targeting moiety that binds specifically to a cell via a cell
 CC surface receptor or antigen thus forming a cell-mutant antibody complex.
 CC On addition of the metal chelate, a cell-antibody-metal chelate complex
 CC is formed that can be detected using emission tomography, magnetic
 CC resonance imaging, lanthanide luminescence, gamma-emissions or single
 CC photon emission tomography (SPET). As such, this method is useful for
 CC treating a subject with cancer and pharmaceutical compositions exhibit
 CC cytostatic and immunosuppressive activities. This polypeptide sequence is
 CC a mutant murine 2D12.5 antibody IgG1 heavy chain variable domain protein,
 CC given in an exemplification of the invention.

XX

SQ Sequence 120 AA;

Query Match 100.0%; Score 638; DB 8; Length 120;
 Best Local Similarity 100.0%; Pred. No. 9.7e-55;
 Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	VKLQESGPGLVQPSQSL SITCTVSGFSLTDYGVHWVRQSPGKGLEWLGVIWSGCGTAYTA	60
Db	3	VKLQESGPGLVQPSQSL SITCTVSGFSLTDYGVHWVRQSPGKGLEWLGVIWSGCGTAYTA	62
Qy	61	AFISRLNIYKD NSKNQVFFEMNSLQADDTAMYYCARRGSYPNYFDVWGQGTTVTVSA	118
Db	63	AFISRLNIYKD NSKNQVFFEMNSLQADDTAMYYCARRGSYPNYFDVWGQGTTVTVSA	120

RESULT 3

ADQ98061

ID ADQ98061 standard; protein; 227 AA.

XX

AC ADQ98061;

XX

DT 21-OCT-2004 (first entry)

XX

DE Chimeric murine N87D G54C 2D12.5 VH antibody fused to human TTCH protein.

XX

KW murine; mouse; chimeric; human; TTCH; tetanus toxin;

KW magnetic resonance imaging; lanthanide luminescence; gamma-emissions;

KW single photon emission tomography; SPET; cancer; cytostatic;

KW immunosuppressive; multi-functional antibody; metal chelate;

KW antigen recognition domain; in vivo imaging;

KW cell-antibody-metal chelate complex; emission tomography; mutant; mutein.

XX
 OS Mus musculus.
 OS Homo sapiens.
 OS Chimeric.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 54
 FT /note= "Wild type Gly substituted for Cys"
 FT Misc-difference 87
 FT /note= "Wild type Asn substituted for Asp"
 XX
 PN WO2004065569-A2.
 XX
 PD 05-AUG-2004.
 XX
 PF 23-JAN-2004; 2004WO-US001808.
 XX
 PR 23-JAN-2003; 2003US-00350555.
 PR 22-JUL-2003; 2003US-00625047.
 PR 31-JUL-2003; 2003US-00631258.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Meares C, Corneillie T;
 XX
 DR WPI; 2004-580725/56.
 DR N-PSDB; ADQ98068.
 XX
 PT Novel mutant antibody comprising reactive site not present in wild-type
 PT of antibody and antigen recognition domain that recognizes macrocyclic
 PT metal chelate having four nitrogen atoms, useful for treating cancer or
 PT autoimmune diseases.
 XX
 PS Claim 41; SEQ ID NO 38; 208pp; English.
 XX
 CC This invention relates to multi-functional antibodies that recognise
 CC chelating agents and metal chelates, particularly macrocyclic metal
 CC chelates. Specifically, it refers to an antibody that comprises a metal
 CC chelate bound to an antigen recognition domain, where the metal chelate
 CC has a reactive functional group of complementary reactivity to the
 CC reactive site of the antibody. This reactive site is the side chain of a
 CC naturally occurring amino acid e.g. the -SH group side chain of a
 CC cysteine residue (not present in the wild type) which can be used to form
 CC a covalent bond between the reactive site of the antibody and the
 CC reactive functional group of the metal chelate. The present invention
 CC describes using these antibodies for in vivo imaging where the antibody
 CC comprises a targeting moiety that binds specifically to a cell via a cell
 CC surface receptor or antigen thus forming a cell-mutant antibody complex.
 CC On addition of the metal chelate, a cell-antibody-metal chelate complex
 CC is formed that can be detected using emission tomography, magnetic
 CC resonance imaging, lanthanide luminescence, gamma-emissions or single
 CC photon emission tomography (SPET). As such, this method is useful for
 CC treating a subject with cancer and pharmaceutical compositions exhibit
 CC cytostatic and immunosuppressive activities. This polypeptide sequence is
 CC the chimeric mutant N87D G54C murine antibody 2D12.5 variable heavy chain
 CC protein fused to the human anti-tetanus toxin antibody CH1 heavy chain

CC constant region of the invention.

XX

SQ Sequence 227 AA;

Query Match 100.0%; Score 638; DB 8; Length 227;
Best Local Similarity 100.0%; Pred. No. 2e-54;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VKLQESGPGGLVQPSQSL SITCTVSGFSLTDYGVHWVRQSPGKGLEWLGVWSGCGTAYTA 60
|||||

Db 3 VKLQESGPGGLVQPSQSL SITCTVSGFSLTDYGVHWVRQSPGKGLEWLGVWSGCGTAYTA 62

Qy 61 AFISRLNIYKDNSKNQVFFEMNSLQADDTAMY YCARRGSYPYNYFDVWGQGTTVTVSA 118
|||||

Db 63 AFISRLNIYKDNSKNQVFFEMNSLQADDTAMY YCARRGSYPYNYFDVWGQGTTVTVSA 120

RESULT 4

ADQ98106

ID ADQ98106 standard; protein; 254 AA.

XX

AC ADQ98106;

XX

DT 21-OCT-2004 (first entry)

XX

DE Chimeric 2dVH-TTCH protein with tag and an N87D/G54C mutations SeqID 84.

XX

KW murine; mouse; chimeric; human; TTCH; tetanus toxin;

KW magnetic resonance imaging; lanthanide luminescence; gamma-emissions;

KW single photon emission tomography; SPET; cancer; cytostatic;

KW immunosuppressive; multi-functional antibody; metal chelate;

KW antigen recognition domain; in vivo imaging;

KW cell-antibody-metal chelate complex; emission tomography; V5 epitope;

KW His tag; mutant; mutein.

XX

OS Mus musculus.

OS Homo sapiens.

OS Chimeric.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 54

FT /note= "Wild type Gly substituted for Cys"

FT Misc-difference 87

FT /note= "Wild type Asn substituted for Asp"

XX

PN WO2004065569-A2.

XX

PD 05-AUG-2004.

XX

PF 23-JAN-2004; 2004WO-US001808.

XX

PR 23-JAN-2003; 2003US-00350555.

PR 22-JUL-2003; 2003US-00625047.

PR 31-JUL-2003; 2003US-00631258.

XX

PA (REGC) UNIV CALIFORNIA.

XX
 PI Meares C, Corneillie T;
 XX
 DR WPI; 2004-580725/56.
 DR N-PSDB; ADQ98099.
 XX
 PT Novel mutant antibody comprising reactive site not present in wild-type
 PT of antibody and antigen recognition domain that recognizes macrocyclic
 PT metal chelate having four nitrogen atoms, useful for treating cancer or
 PT autoimmune diseases.
 XX
 PS Claim 41; SEQ ID NO 83; 208pp; English.
 XX
 CC This invention relates to multi-functional antibodies that recognise
 CC chelating agents and metal chelates, particularly macrocyclic metal
 CC chelates. Specifically, it refers to an antibody that comprises a metal
 CC chelate bound to an antigen recognition domain, where the metal chelate
 CC has a reactive functional group of complementary reactivity to the
 CC reactive site of the antibody. This reactive site is the side chain of a
 CC naturally occurring amino acid e.g. the -SH group side chain of a
 CC cysteine residue (not present in the wild type) which can be used to form
 CC a covalent bond between the reactive site of the antibody and the
 CC reactive functional group of the metal chelate. The present invention
 CC describes using these antibodies for in vivo imaging where the antibody
 CC comprises a targeting moiety that binds specifically to a cell via a cell
 CC surface receptor or antigen thus forming a cell-mutant antibody complex.
 CC On addition of the metal chelate, a cell-antibody-metal chelate complex
 CC is formed that can be detected using emission tomography, magnetic
 CC resonance imaging, lanthanide luminescence, gamma-emissions or single
 CC photon emission tomography (SPET). As such, this method is useful for
 CC treating a subject with cancer and pharmaceutical compositions exhibit
 CC cytostatic and immunosuppressive activities. This polypeptide is the
 CC mutant protein sequence comprising a chimeric murine antibody 2D12.5
 CC variable heavy chain protein fused to the human anti-tetanus toxin
 CC antibody CH1 heavy chain constant region (2dVH-TTCH) with N87D and G54C
 CC mutations and a V5 epitope with (His)6 tag, given in an exemplification
 CC of the invention.
 XX
 SQ Sequence 254 AA;

Query Match 100.0%; Score 638; DB 8; Length 254;
 Best Local Similarity 100.0%; Pred. No. 2.2e-54;
 Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VKLQESGPGLVQPSQSL SITCTVSGFSLTDYGVHWVRQSPGKGLEWLGVIWSGCGTAYTA 60
 ||||||||||||||||||
 Db 3 VKLQESGPGLVQPSQSL SITCTVSGFSLTDYGVHWVRQSPGKGLEWLGVIWSGCGTAYTA 62
 Qy 61 AFISRLNIYKD NSKNQVFFEMNSLQADDTAMYYCARRGSPYNYFDVWGQGT TTVTVSA 118
 ||||||||||||||||||
 Db 63 AFISRLNIYKD NSKNQVFFEMNSLQADDTAMYYCARRGSPYNYFDVWGQGT TTVTVSA 120

RESULT 5
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 ID ADQ98034 standard; protein; 118 AA.
 XX

AC ADQ98034;
XX
DT 21-OCT-2004 (first entry)
XX
DE Mutant murine antibody 2D12.5 variable heavy chain protein N87D Seq 11.
XX
KW murine; mouse; mutant; mutein; antigen recognition domain;
KW in vivo imaging; cell-antibody-metal chelate complex;
KW emission tomography; magnetic resonance imaging; lanthanide luminescence;
KW gamma-emissions; single photon emission tomography; SPET; cancer;
KW cytostatic; immunosuppressive; multi-functional antibody; metal chelate.
XX
OS Mus musculus.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 87
FT /note= "Wild type Asn substituted for Asp"
XX
PN WO2004065569-A2.
XX
PD 05-AUG-2004.
XX
PF 23-JAN-2004; 2004WO-US001808.
XX
PR 23-JAN-2003; 2003US-00350555.
PR 22-JUL-2003; 2003US-00625047.
PR 31-JUL-2003; 2003US-00631258.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Meares C, Corneillie T;
XX
DR WPI; 2004-580725/56.
DR N-PSDB; ADQ98040.
XX
PT Novel mutant antibody comprising reactive site not present in wild-type
PT of antibody and antigen recognition domain that recognizes macrocyclic
PT metal chelate having four nitrogen atoms, useful for treating cancer or
PT autoimmune diseases.
XX
PS Claim 41; SEQ ID NO 11; 208pp; English.
XX
CC This invention relates to multi-functional antibodies that recognise
CC chelating agents and metal chelates, particularly macrocyclic metal
CC chelates. Specifically, it refers to an antibody that comprises a metal
CC chelate bound to an antigen recognition domain, where the metal chelate
CC has a reactive functional group of complementary reactivity to the
CC reactive site of the antibody. This reactive site is the side chain of a
CC naturally occurring amino acid e.g. the -SH group side chain of a
CC cysteine residue (not present in the wild type) which can be used to form
CC a covalent bond between the reactive site of the antibody and the
CC reactive functional group of the metal chelate. The present invention
CC describes using these antibodies for in vivo imaging where the antibody
CC comprises a targeting moiety that binds specifically to a cell via a cell
CC surface receptor or antigen thus forming a cell-mutant antibody complex.
CC On addition of the metal chelate, a cell-antibody-metal chelate complex

us-10-631-258-13.rapb

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OM protein - protein search, using sw model

Run on: June 8, 2005, 15:39:42 ; Search time 1892 Seconds
(without alignments)
23.908 Million cell updates/sec

Title: US-10-631-258-13
Perfect score: 638
Sequence: 1 VKLQESGPGLVQPSQSL SIT.....SYPYNYFDVWGQTTVTVSA 118

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1710399 seqs, 383334425 residues

Total number of hits satisfying chosen parameters: 1710399

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*

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- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	638	100.0	118	16	US-10-625-047-13	Sequence 13, Appl

us-10-631-258-13.rapb						
2	638	100.0	118	17	US-10-631-258-13	Sequence 13, Appl
3	638	100.0	227	16	US-10-625-047-38	Sequence 38, Appl
4	638	100.0	227	17	US-10-631-258-38	Sequence 38, Appl
5	626	98.1	118	16	US-10-625-047-11	Sequence 11, Appl
6	626	98.1	118	17	US-10-631-258-11	Sequence 11, Appl
7	626	98.1	227	16	US-10-625-047-36	Sequence 36, Appl
8	626	98.1	227	17	US-10-631-258-36	Sequence 36, Appl
9	621	97.3	118	16	US-10-625-047-10	Sequence 10, Appl
10	621	97.3	118	17	US-10-631-258-10	Sequence 10, Appl
11	621	97.3	227	16	US-10-625-047-35	Sequence 35, Appl
12	621	97.3	227	16	US-10-625-047-40	Sequence 40, Appl
13	621	97.3	227	17	US-10-631-258-35	Sequence 35, Appl
14	621	97.3	227	17	US-10-631-258-40	Sequence 40, Appl
15	618	96.9	118	16	US-10-625-047-9	Sequence 9, Appli
16	618	96.9	118	16	US-10-625-047-41	Sequence 41, Appl
17	618	96.9	118	17	US-10-631-258-9	Sequence 9, Appli
18	618	96.9	118	17	US-10-631-258-41	Sequence 41, Appl
19	618	96.9	119	16	US-10-625-047-5	Sequence 5, Appli
20	618	96.9	119	17	US-10-631-258-5	Sequence 5, Appli
21	617	96.7	118	16	US-10-625-047-12	Sequence 12, Appl
22	617	96.7	118	16	US-10-625-047-14	Sequence 14, Appl
23	617	96.7	118	17	US-10-631-258-12	Sequence 12, Appl
24	617	96.7	118	17	US-10-631-258-14	Sequence 14, Appl
25	617	96.7	227	16	US-10-625-047-37	Sequence 37, Appl
26	617	96.7	227	16	US-10-625-047-39	Sequence 39, Appl
27	617	96.7	227	17	US-10-631-258-37	Sequence 37, Appl
28	617	96.7	227	17	US-10-631-258-39	Sequence 39, Appl
29	607	95.1	116	17	US-10-854-735-13	Sequence 13, Appl
30	607	95.1	116	17	US-10-835-533-13	Sequence 13, Appl
31	595	93.3	116	17	US-10-854-735-11	Sequence 11, Appl
32	595	93.3	116	17	US-10-835-533-11	Sequence 11, Appl
33	590	92.5	116	17	US-10-854-735-10	Sequence 10, Appl
34	590	92.5	116	17	US-10-835-533-10	Sequence 10, Appl
35	587	92.0	116	17	US-10-854-735-9	Sequence 9, Appli
36	587	92.0	116	17	US-10-835-533-9	Sequence 9, Appli
37	587	92.0	117	17	US-10-854-735-5	Sequence 5, Appli
38	587	92.0	117	17	US-10-835-533-5	Sequence 5, Appli
39	586	91.8	116	17	US-10-854-735-12	Sequence 12, Appl
40	586	91.8	116	17	US-10-854-735-14	Sequence 14, Appl
41	586	91.8	116	17	US-10-835-533-12	Sequence 12, Appl
42	586	91.8	116	17	US-10-835-533-14	Sequence 14, Appl
43	498.5	78.1	116	16	US-10-682-845-53	Sequence 53, Appl
44	498.5	78.1	492	16	US-10-682-845-59	Sequence 59, Appl
45	498.5	78.1	492	16	US-10-682-845-61	Sequence 61, Appl

ALIGNMENTS

```

RESULT 1
US-10-625-047-13
; Sequence 13, Application US/10625047
; Publication No. US20040198962A1
; GENERAL INFORMATION:
; APPLICANT: Meares, Claude
; APPLICANT: Corneillie, Todd
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Multi-Functional Antibodies
; FILE REFERENCE: 023070-130910US
; CURRENT APPLICATION NUMBER: US/10/625,047
; CURRENT FILING DATE: 2003-07-22
; PRIOR APPLICATION NUMBER: US 10/350,555
; PRIOR FILING DATE: 2003-01-23

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; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
;   LENGTH: 118
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:N87D G54C
;   OTHER INFORMATION: cloned mutant murine 2D12.5 heavy chain variable
;   OTHER INFORMATION: region (VH)
US-10-625-047-13

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Qy 1 VKLQESGPGLVQPSQSL SITCTVSGFSLTDYGVHWVRQSPGKGLEWL GVIWSGCGTAYTA 60
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Db 1 VKLQESGPGLVQPSQSL SITCTVSGFSLTDYGVHWVRQSPGKGLEWL GVIWSGCGTAYTA 60

Qy 61 AFISRLNIYKDNSKNQVFFEMNSLQADDTAMYYCARRGSYPYNYFDVWGQGTTVTVSA 118
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Db 61 AFISRLNIYKDNSKNQVFFEMNSLQADDTAMYYCARRGSYPYNYFDVWGQGTTVTVSA 118

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; Sequence 13, Application US/10631258
; Publication No. US20050026263A1
; GENERAL INFORMATION:
; APPLICANT: Meares, Claude
; APPLICANT: Corneillie, Todd
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Multi-Functional Antibodies
; FILE REFERENCE: 023070-130920US
; CURRENT APPLICATION NUMBER: US/10/631,258
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: US 10/350,555
; PRIOR FILING DATE: 2003-01-23
; PRIOR APPLICATION NUMBER: US 10/625,047
; PRIOR FILING DATE: 2003-07-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: cloned mutant murine 2D12.5 heavy c
; OTHER INFORMATION: region (VH)

```

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Qy      1 VKLQESGPGLVQPSQSL SITCTVSGFSLTDYGVHWVRQSPGKGLEWLGVIWSGCGTAYTA 60
        |||
Db      1 VKLQESGPGLVQPSQSL SITCTVSGFSLTDYGVHWVRQSPGKGLEWLGVIWSGCGTAYTA 60
        |||

Qy     61 AFISRLNIYKDNSKNQVFFEMNSLQADDTAMYYCARRGSYPYNYFDVWGQGTTVTVSA 118
        |||

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Db 61 AFISRLNIYKDNSKNQVFFEMNSLQADDTAMYYCARRGSYPYNYFDVWGQGTTTVTVSA 118

RESULT 3

US-10-625-047-38

; Sequence 38, Application US/10625047

; Publication No. US20040198962A1

; GENERAL INFORMATION:

; APPLICANT: Meares, Claude

; APPLICANT: Corneillie, Todd

; APPLICANT: The Regents of the University of California

; TITLE OF INVENTION: Multi-Functional Antibodies

; FILE REFERENCE: 023070-130910US

; CURRENT APPLICATION NUMBER: US/10/625,047

; CURRENT FILING DATE: 2003-07-22

; PRIOR APPLICATION NUMBER: US 10/350,555

; PRIOR FILING DATE: 2003-01-23

; NUMBER OF SEQ ID NOS: 72

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 38

; LENGTH: 227

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:N87D G54C

; OTHER INFORMATION: cloned mutant chimeric murine 2D12.5 heavy chain

; OTHER INFORMATION: variable region (VH) fused to human anti-tetanus

; OTHER INFORMATION: toxin antibody CH1 heavy chain constant region

; OTHER INFORMATION: (TTCH)

US-10-625-047-38

Query Match 100.0%; Score 638; DB 16; Length 227;

Best Local Similarity 100.0%; Pred. No. 9.4e-53;

Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VKLQESGPGLVQPSQSL SITCTVSGFSLTDYGVHWVRQSPGKGLEWLGVIWSGCGTAYTA 60

Db 3 VKLQESGPGLVQPSQSL SITCTVSGFSLTDYGVHWVRQSPGKGLEWLGVIWSGCGTAYTA 62

Qy 61 AFISRLNIYKDNSKNQVFFEMNSLQADDTAMYYCARRGSYPYNYFDVWGQGTTTVTVSA 118

Db 63 AFISRLNIYKDNSKNQVFFEMNSLQADDTAMYYCARRGSYPYNYFDVWGQGTTTVTVSA 120

RESULT 4

US-10-631-258-38

; Sequence 38, Application US/10631258

; Publication No. US20050026263A1

; GENERAL INFORMATION:

; APPLICANT: Meares, Claude

; APPLICANT: Corneillie, Todd

; APPLICANT: The Regents of the University of California

; TITLE OF INVENTION: Multi-Functional Antibodies

; FILE REFERENCE: 023070-130920US

; CURRENT APPLICATION NUMBER: US/10/631,258

; CURRENT FILING DATE: 2003-07-31

; PRIOR APPLICATION NUMBER: US 10/350,555

; PRIOR FILING DATE: 2003-01-23

; PRIOR APPLICATION NUMBER: US 10/625,047

; PRIOR FILING DATE: 2003-07-22

; NUMBER OF SEQ ID NOS: 72

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 38

OM protein - protein search, using sw model

Run on: June 8, 2005, 15:15:54 ; Search time 41 Seconds
 (without alignments)
 276.917 Million cell updates/sec

Title: US-10-631-258-13
 Perfect score: 638
 Sequence: 1 VKLQESGPGGLVQPSQSL SIT.....SYPYNYFDVWGQGTTVTVSA 118

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : PIR_79:*
 1: pirl:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		DB	ID	Description
	Score	Match Length			
1	496.5	77.8	135	2	S31913 Ig gamma-2A chain
2	487	76.3	127	2	B31807 Ig heavy chain V r
3	480	75.2	140	2	S14238 Ig gamma-1 chain p
4	479	75.1	114	2	S26321 Ig heavy chain V r
5	472.5	74.1	115	2	S26470 Ig heavy chain V r
6	466	73.0	121	2	D30560 Ig heavy chain V r
7	462	72.4	121	2	S33131 Ig heavy chain V r
8	458	71.8	115	2	S11107 Ig heavy chain V r
9	453	71.0	140	2	S55028 Ig heavy chain V r
10	452	70.8	116	2	PL0198 anti-DNA autoantib
11	452	70.8	118	2	PQ0266 Ig heavy chain V r
12	450.5	70.6	116	2	S42484 Ig heavy chain V r
13	450.5	70.6	117	2	S38563 Ig heavy chain V r

14	449	70.4	109	2	PH1026	Ig heavy chain V r
15	448	70.2	112	2	S11100	Ig heavy chain V r
16	448	70.2	231	2	PC4155	Ig gamma-2b chain
17	447	70.1	114	2	S11106	Ig heavy chain V r
18	446.5	70.0	122	2	A49049	Ig heavy chain V r
19	446	69.9	116	2	S11102	Ig heavy chain V r
20	444.5	69.7	139	2	A32456	Ig heavy chain pre
21	444	69.6	113	2	S11101	Ig heavy chain V r
22	440.5	69.0	141	2	S52446	Ig heavy chain V r
23	436	68.3	116	2	A33932	Ig mu chain precu
24	433.5	67.9	118	2	S32786	Ig heavy chain (an
25	433.5	67.9	120	2	PL0087	Ig heavy chain V r
26	433	67.9	115	2	S11103	Ig heavy chain V r
27	433	67.9	116	1	G1MS10	Ig heavy chain pre
28	432	67.7	106	2	S26322	Ig heavy chain V r
29	431.5	67.6	122	2	S20809	Ig heavy chain V r
30	431	67.6	100	2	A25913	Ig heavy chain pre
31	431	67.6	114	2	S11099	Ig heavy chain V r
32	429	67.2	112	2	S11108	Ig heavy chain V r
33	425	66.6	90	2	A49042	Ig heavy chain V r
34	425	66.6	144	1	G2MS14	Ig heavy chain pre
35	418.5	65.6	107	2	S14506	Ig heavy chain V r
36	418.5	65.6	144	2	S11244	Ig gamma-2a chain
37	417	65.4	114	2	S11105	Ig heavy chain V r
38	412	64.6	117	2	S10111	Ig heavy chain V r
39	411	64.4	112	2	S11098	Ig heavy chain V r
40	411	64.4	114	2	S11104	Ig heavy chain V r
41	410.5	64.3	107	2	S14492	Ig heavy chain V r
42	407	63.8	106	2	S14489	Ig heavy chain V r
43	407	63.8	111	2	S26324	Ig heavy chain V r
44	406.5	63.7	107	2	S14493	Ig heavy chain V r
45	405.5	63.6	107	2	S14491	Ig heavy chain V r

ALIGNMENTS

RESULT 1

S31913

Ig gamma-2A chain precursor - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_change 23-Jul-1999

C;Accession: S31913

R;Bespalov, I.A.; Hiyanov, P.A.; Lukashevich, L.V.; Lunev, V.E.; Tribush, S.S.; Gaponova, G.I.; Deyev, S.M.

submitted to the EMBL Data Library, January 1993

A;Reference number: S31913

A;Accession: S31913

A;Molecule type: mRNA

A;Residues: 1-135 <BES>

A;Cross-references: EMBL:X70822; NID:g57921; PIDN:CAA50153.1; PID:g57922

A;Experimental source: strain BALB/c

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;1-11/Domain: signal sequence #status predicted <SIG>

F;12-135/Product: Ig gamma-2A chain (fragment) #status predicted <MAT>

F;34-116/Domain: immunoglobulin homology <IMM>

Query Match 77.8%; Score 496.5; DB 2; Length 135;
Best Local Similarity 80.5%; Pred. No. 3.6e-40;
Matches 95; Conservative 10; Mismatches 10; Indels 3; Gaps 1;

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Qy      1 VKLQESGPGLVQPSQSL SITCTVSGFSLTDYGVHWVRQSPGKGLEWLGVIWSGCGTAYTA 60
      |:|:|:|||||
Db      21 VQLKQSGPGLVQPSQSL SITCTVSGFSLTSYGVHWVRQSPGKGLEWLGVIWSGGSTDYNA 80

Qy      61 AFISRLNIYKDNSKNQVFFEMNSLQADDTAMYYCARRGSYPYNYFDVWGQGTTVTVSA 118
      |||||:| |||||:||||:|||||:|||:|||| | ||| |||||:|||:
Db      81 AFISRLSISKDNSKSQVFFKMNSLQANDTAIYYCARELVY---YFDYWGGGTTTLTVSS 135

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RESULT 2

B31807

Ig heavy chain V region (PAC1) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 20-Jul-1989 #sequence revision 20-Jul-1989 #text change 23-May-1997

C;Accession: B31807

R;Taub, R.; Gould, R.J.; Garsky, V.M.; Ciccarone, T.M.; Hoxie, J.; Friedman, P.A.; Shattil, S.J.

J. Biol. Chem. 264, 259-265, 1989

A;Title: A monoclonal antibody against the platelet fibrinogen receptor contains a sequence that mimics a receptor recognition domain in fibrinogen.

A;Reference number: A31807; MUID:89079661; PMID:2909518

A;Accession: B31807

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-127 <TAU>

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-97/Domain: immunoglobulin homology <IMM>

Query Match 76.3%; Score 487; DB 2; Length 127;
Best Local Similarity 74.6%; Pred. No. 2.7e-39;
Matches 94; Conservative 11; Mismatches 13; Indels 8; Gaps 1;

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Qy      1 VKLQESGPGLVQPSQSLSITCTVSGFSLTDYGVHWVRQSPGKGLEWLGVIWSGC GTAYTA 60  
        |:|::||| | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db      2 VQLKQSGPGLVQPSQSLSITCTVSGFSLTSYGVHWRRLSPGKGLEWLGVIWSGGSTDYNA 61  
  
Qy     61 AFISRLNIYKDNSKNQVFFEMNSLQADDTAMYYCARR-----GSYPNYFDVWGQGT 112  
        |||||:| |||||:|||:|||||:| | :||| | | | | | | | | | | | |  
Db     62 AFISRLSISKDNSKSQVFFKMNSLQANDTGIYYCARRSPSYRYDGAGPYAMDYWGQGT 121  
  
Qy    113 TVTVSA 118  
        :|||:  
Db    122 SVTVSS 127
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us-10-631-258-13.rup

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 8, 2005, 13:18:42 ; Search time 123 Seconds
(without alignments)
491.263 Million cell updates/sec

Title: US-10-631-258-13
Perfect score: 638
Sequence: 1 VKLQESGPGLVQPSQSL SIT.....SYPYNYFDVWGQTTVTVSA 118

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	433	67.9	116	1	HV45_MOUSE	P01821 mus musculu
2	425	66.6	144	1	HV43_MOUSE	P01819 mus musculu
3	423.5	66.4	121	2	Q99NG4	Q99ng4 mus musculu
4	417.5	65.4	482	2	Q91X92	Q91x92 mus musculu
5	378	59.2	115	1	HV44_MOUSE	P01820 mus musculu
6	374.5	58.7	135	1	HV02_XENLA	P20957 xenopus lae
7	359.5	56.3	573	2	Q8WU38	Q8wu38 homo sapien
8	358	56.1	472	2	Q6N089	Q6n089 homo sapien
9	348.5	54.6	136	1	HV16_MOUSE	P01783 mus musculu
10	348	54.5	119	2	Q9UL73	Q9ul73 homo sapien
11	347.5	54.5	613	2	Q8WUK1	Q8wuk1 homo sapien
12	341	53.4	476	2	Q6GMX1	Q6gmx1 homo sapien
13	336	52.7	492	2	Q7Z374	Q7z374 homo sapien
14	335.5	52.6	122	2	Q9UL84	Q9ul84 homo sapien
15	335	52.5	136	1	HV01_XENLA	P20956 xenopus lae
16	335	52.5	493	2	Q8NCL6	Q8ncl6 homo sapien
17	333.5	52.3	478	2	Q7Z379	Q7z379 homo sapien
18	332	52.0	479	2	Q99M22	Q99m22 mus musculu
19	331	51.9	121	1	HV3J_HUMAN	P01771 homo sapien
20	331	51.9	121	2	Q9UL71	Q9ul71 homo sapien
21	331	51.9	137	1	HV46_MOUSE	P01822 mus musculu

					us-10-631-258-13.rup	
22	329.5	51.6	136	2	Q6LBQ5	Q6lbq5 mus musculu
23	329.5	51.6	465	2	Q6GMX6	Q6gmx6 homo sapien
24	329	51.6	116	2	Q9UL93	Q9ul93 homo sapien
25	328.5	51.5	477	2	Q6GMX7	Q6gmx7 homo sapien
26	327.5	51.3	606	2	Q6GMY2	Q6gmy2 homo sapien
27	327	51.3	499	2	Q8N5K4	Q8n5k4 homo sapien
28	326.5	51.2	119	1	HV38_MOUSE	P01808 mus musculu
29	326.5	51.2	484	2	Q8VEA0	Q8vea0 mus musculu
30	326	51.1	470	2	Q6PJA4	Q6pja4 homo sapien
31	325.5	51.0	112	2	Q9HCC1	Q9hcc1 homo sapien
32	323	50.6	240	2	Q65ZC9	Q65zc9 homo sapien
33	323	50.6	478	2	Q6PI81	Q6pi81 homo sapien
34	322.5	50.5	118	2	Q9UL91	Q9ul91 homo sapien
35	322.5	50.5	576	2	Q6P4I8	Q6p4i8 homo sapien
36	321.5	50.4	473	2	Q91Z05	Q91z05 mus musculu
37	321	50.3	487	2	Q80ZI7	Q80zi7 mus musculu
38	320.5	50.2	119	1	HV40_MOUSE	P01810 mus musculu
39	320	50.2	113	2	Q9UL90	Q9ul90 homo sapien
40	320	50.2	485	2	Q6PDB8	Q6pdb8 mus musculu
41	318.5	49.9	122	1	HV3G_HUMAN	P01768 homo sapien
42	318.5	49.9	475	2	Q6MZQ6	Q6mzq6 homo sapien
43	318	49.8	121	2	Q9UL96	Q9ul96 homo sapien
44	317	49.7	255	2	Q6KB05	Q6kb05 mus musculu
45	316.5	49.6	473	2	Q6MZV7	Q6mzv7 homo sapien

ALIGNMENTS

RESULT 1

HV45_MOUSE

ID HV45_MOUSE STANDARD; PRT; 116 AA.

AC P01821;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Ig heavy chain V region MC101 precursor.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=82075900; PubMed=6273429;

RA Kataoka T., Nikaido T., Miyata T., Moriwaki K., Honjo T.;

RT "The nucleotide sequences of rearranged and germline immunoglobulin VH

RT genes of a mouse myeloma MC101 and evolution of VH genes in mouse.";

RL J. Biol. Chem. 257:277-285(1982).

CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.

CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC use by non-profit institutions as long as its content is in no way
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 CC or send an email to license@isb-sib.ch).
 CC -----

DR EMBL; J00502; AAA38515.1; -.

DR PIR; A02096; G1MS10.

DR HSSP; P01820; 1G7J.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig_v.


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DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL          1          19
FT   CHAIN           20        116      Ig heavy chain V region MC101.
FT   DOMAIN          20        >116     Ig-like.
FT   NON_TER         116        116
SQ   SEQUENCE        116 AA;  12593 MW;  8079A6EE7C552B3E CRC64;

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Qy      1 VKLQESGPGLVQPSQSL SITCTVSGFSLTDYGVHWVRQSPGKGLEWLGVIWSGCGTAYTA 60
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Db     21 VQLKQSGPGLVQPSQSL SITCTVSGFSLTSYGVHWVRQSPGKGLEWLGVIWSGGSTDYNA 80
      |||||:| |||||:|||||:|||||:|
Qy     61 AFISRLNIYKDNSKNQVFFEMNSLQADDTAMYYCAR 96
      |||||:| |||||:|||||:|||||:|
Db     81 AFISRLSISKDNSKSQVFFKMNSLQSNDAIYYCAR 116

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ID      HV43_MOUSE          STANDARD;          PRT;          144 AA.
AC      P01819;
DT      21-JUL-1986 (Rel. 01, Created)
DT      21-JUL-1986 (Rel. 01, Last sequence update)
DT      29-MAR-2004 (Rel. 43, Last annotation update)
DE      Ig heavy chain V region MOPC 141 precursor.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=81012133; PubMed=6774258;
RA      Sakano H., Maki R., Kurosawa Y., Roeder W., Tonegawa S.;
RT      "Two types of somatic recombination are necessary for the generation
RT      of complete immunoglobulin heavy-chain genes.";
RL      Nature 286:676-683(1980).
CC      -!- MISCELLANEOUS: The sequence shown is translated from a
CC      differentiated gene isolated from a myeloma that secretes IgG2b.
CC      -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; J00491; AAA38121.1; -.
DR      PIR; A02094; G2MS14.
DR      HSSP; P01820; 1G7J.
DR      InterPro; IPR007110; Ig-like.
DR      InterPro; IPR003596; Ig_v.
DR      Pfam; PF00047; ig; 1.
DR      SMART; SM00406; IGv; 1.
DR      PROSITE; PS50835; IG_LIKE; 1.
KW      Immunoglobulin V region; Signal.

```

us-10-631-258-13.rup

FT	SIGNAL	1	19	
FT	CHAIN	20	144	Ig heavy chain V region MOPC 141.
FT	DOMAIN	20	130	Ig-like.
FT	NON_TER	144	144	
SQ	SEQUENCE	144 AA;	15759 MW;	8E47A7CB3706D30A CRC64;

Query Match 66.6%; Score 425; DB 1; Length 144;
Best Local Similarity 68.5%; Pred. No. 8.5e-36;
Matches 85; Conservative 8; Mismatches 25; Indels 6; Gaps 2;

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Qy      1 VKLQESGPGPLVQPSQSL SITCTVSGFSLTDYGVHWVRQSPGKGLEWLGVIWSGC GTAYTA 60
        |:|:||||||| ||||| ||||| ||||| ||||| :||| | ||||| ||| | | :
Db     21 VQLKESGPGPLVAPSQSL SITCTVSGFSLTGYGVNWVRQPPGKGLEWLGTIWGN GSTDYN S 80

Qy     61 AFISRLNIYKD NSKNQVFFEMNSL QADDTAMYYCARRGSYPY----NYF--DVWGQGTTV 114
        ||| | |||||:||| :||| | ||||| ||||| | | | | ||| | |||||:|
Db    81 TLKSRLTITKDNSKSQVFLKMNSLQTDDTARYYCASVSIYYYGRSDKYFTLDYW GQGTSV 140

Qy     115 TVSA 118
        |||:
Db    141 TVSS 144
```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 8, 2005, 15:48:17 ; Search time 2267 Seconds
(without alignments)
2522.151 Million cell updates/sec

Title: US-10-631-258-13
Perfect score: 638
Sequence: 1 VKLQESGPGLVQPSQSL SIT.....SYPYNYFDVWGQGTTVTVSA 118

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10631258 @CGN_1_1_5600 @runat_07062005_122948_29497 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*

1:	gb_ba:*
2:	gb_htg:*
3:	gb_in:*
4:	gb_om:*
5:	gb_ov:*
6:	gb_pat:*
7:	gb_ph:*
8:	gb_pl:*
9:	gb_pr:*
10:	gb_ro:*

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11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query Match	Length	DB	ID	Description	
1	507.5	79.5	408	10	MUSN	L23131 Mus musculu	
2	503	78.8	489	10	AY436968	AY436968 Mus muscu	
3	499	78.2	798	6	AR121619	AR121619 Sequence	
4	499	78.2	810	6	A41894	A41894 Sequence 2	
5	498.5	78.1	345	10	MMU01353	U01353 Mus musculu	
6	498.5	78.1	366	10	MMAHCVD	X58292 M.musculus	
7	498.5	78.1	450	10	AY436954	AY436954 Mus muscu	
8	498	78.1	381	10	MUSIGHLS	J04439 Mouse Ig-mu	
9	498	78.1	594	10	S59883	S59883 IgH VDJ [mi	
10	497.5	78.0	354	10	MUSIGHMNA	L19122 Mouse Ig re	
11	497.5	78.0	1371	6	BD222935	BD222935 Heteromin	
12	497.5	78.0	1371	6	AX023359	AX023359 Sequence	
13	497.5	78.0	1380	6	CQ856167	CQ856167 Sequence	
14	497.5	78.0	1389	6	BD222936	BD222936 Heteromin	
15	497.5	78.0	1389	6	AX023361	AX023361 Sequence	
16	496.5	77.8	414	10	MMIGG2A	X70822 M.musculus	
17	496.5	77.8	492	10	MMU26995	U26995 Mus musculu	
18	495.5	77.7	417	10	MUSIHCC	L41878 Mus musculu	
19	493	77.3	339	10	AY182545	AY182545 Mus muscu	
20	492.5	77.2	419	10	MUSIGMD23A	M27107 Mus musculu	
21	491.5	77.0	360	10	AF163756	AF163756 Mus muscu	
22	491	77.0	453	10	AY454499	AY454499 Mus muscu	
23	490.5	76.9	354	10	AY436943	AY436943 Mus muscu	
24	490.5	76.9	384	10	AF072885	AF072885 Mus muscu	
25	490	76.8	357	10	MDIGGVAL	Z22047 M.domesticu	
26	490	76.8	414	6	AR126845	AR126845 Sequence	
27	490	76.8	414	6	I31940	I31940 Sequence 32	
28	490	76.8	414	6	I78552	I78552 Sequence 32	
29	490	76.8	414	6	I78607	I78607 Sequence 32	
30	490	76.8	414	10	MUSABIL2RH	L06840 Mus musculu	
31	490	76.8	471	10	MUSIGH1NP	M26981 Mus musculu	
32	490	76.8	747	10	S46670	S46670 immunotoxin	
33	489	76.6	351	10	AF178587	AF178587 Mus muscu	
34	489	76.6	738	10	MMU345034	AJ345034 Mus muscu	
35	488.5	76.6	336	10	MUSIGMRNAG	L21022 Mus musculu	
36	488.5	76.6	342	6	AR453129	AR453129 Sequence	
37	488.5	76.6	342	10	AF287274	AF287274 Mus muscu	
38	488.5	76.6	363	10	AY436941	AY436941 Mus muscu	
39	488	76.5	369	10	AY550917	AY550917 Mus muscu	
40	487	76.3	381	6	I08253	I08253 Sequence 3	
41	485.5	76.1	405	10	AF099087	AF099087 Mus muscu	
42	484.5	75.9	405	10	AF281861	AF281861 Mus muscu	

43	484.5	75.9	1632	12	SYN507107	AJ507107 Synthetic
44	484.5	75.9	1701	12	SCO564232	AJ564232 Synthetic
45	484	75.9	351	10	AY229949	AY229949 Mus muscu

ALIGNMENTS

RESULT 1

MUSN

LOCUS MUSN 408 bp mRNA linear ROD 14-MAR-1994

DEFINITION Mus musculus immunoglobulin heavy chain (IgH) mRNA,VDJ1 region, partial cds.

ACCESSION L23131

VERSION L23131.1 GI:393173

KEYWORDS Ig heavy chain; diversity region; immunoglobulin; joining region; variable region.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 408)

AUTHORS Sheehan,K.M., Mainville,C.A., Willert,S. and Brodeur,P.H.

TITLE The utilization of individual VH exons in the primary repertoire of

adult BALB/c mice

JOURNAL J. Immunol. 151 (10), 5364-5375 (1993)

MEDLINE 94044761

PUBMED 8228231

COMMENT Original source text: Mus musculus (strain BALB/cByJ) female adult spleen cDNA to mRNA.

FEATURES Location/Qualifiers

source

1. .408
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/mol_type="mRNA"
/strain="BALB/cByJ"
/db_xref="taxon:10090"
/map="chromosome 12"
/sex="female"
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/dev_stage="adult"

gene

1. .408
/gene="IgH"

CDS

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/protein_id="AAA16775.1"
/db_xref="GI:393174"

/translation="LELLLSLVTFPSCVLSQVQMKQSGPGLVQPSQSL SITCTVSGFS

LTSYGVHWVRQSPGKGLEWLGVIWGGSTDYNAAFISRLSISKDNSKSQVFFKMNSLQ

ADDTAIYYCARLGIYYDLWYFDVWGAGTTVTVSS"

V_region

1. .339

/gene="IgH"

ORIGIN

Alignment Scores:

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Score:	507.50	Matches:	98
Percent Similarity:	90.00%	Conservative:	10
Best Local Similarity:	81.67%	Mismatches:	9
Query Match:	79.55%	Indels:	3
DB:	10	Gaps:	2

US-10-631-258-13 (1-118) x MUSN (1-408)

Qy	1	VallLysLeuGlnGluSerGlyProGlyLeuValGlnProSerGlnSerLeuSerIleThr	20
		:::	
Db	52	GTGCAGATGAAGCAGTCAGGACCTGGCCTAGTGCAGCCCTCACAGAGCCTGTCCATCACC	111
Qy	21	CysThrValSerGlyPheSerLeuThrAspTyrGlyValHisTrpValArgGlnSerPro	40
Db	112	TGCACAGTCTCTGGTTTCTCATTAAGTATGGTGTACACTGGGTTCGCCAGTCTCCA	171
Qy	41	GlyLysGlyLeuGluTrpLeuGlyValIleTrpSerGlyCysGlyThrAlaTyrThrAla	60
Db	172	GGAAAGGGTCTGGAGTGGCTGGGAGTGATATGGAGTGGTGGGAAGCACAGACTATAATGCA	231
Qy	61	AlaPheIleSerArgLeuAsnIleTyrLysAspAsnSerLysAsnGlnValPhePheGlu	80
		:::	
Db	232	GCTTTCATATCCAGACTGAGCATCAGCAAGGACAAGTCCAGAGCCAAGTTTCTTTAAA	291
Qy	81	MetAsnSerLeuGlnAlaAspAspThrAlaMetTyrTyrCysAlaArgArgGlySerTyr	100
		:::	
Db	292	ATGAACAGTCTGCAAGCTGATGACACAGCCATATACTACTGTGCCAGATTGGGAATCTAC	351
Qy	101	ProTyrAsn-----TyrPheAspValTrpGlyGlnGlyThrThrValThrValSerAla	118
		:::	
Db	352	---TATGACCTCTGGTACTTCGATGTCTGGGGCGCAGGGACCACGGTCACCGTCTCCTCA	408

RESULT 2

AY436968

LOCUS AY436968 489 bp DNA linear ROD 15-MAR-2004

DEFINITION Mus musculus ZB9D4 ANA immunoglobulin heavy chain gene, partial cds.

ACCESSION AY436968

VERSION AY436968.1 GI:40794884

KEYWORDS .

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 489)

AUTHORS Liang,Z., Xie,C., Chen,C., Kreska,D., Hsu,K., Li,L., Zhou,X.J. and Mohan,C.

TITLE Pathogenic Profiles and Molecular Signatures of Antinuclear Autoantibodies Rescued from NZM2410 Lupus Mice

JOURNAL J. Exp. Med. 199 (3), 381-398 (2004)

PUBMED 14757744
REFERENCE 2 (bases 1 to 489)
AUTHORS Liang,Z., Xie,C., Chen,C., Kreska,D., Hsu,K., Li,L., Zhou,J.X. and Mohan,C.
TITLE Direct Submission
JOURNAL Submitted (29-SEP-2003) Simmons Arthritis Research Center and Center for Immunology, University of Texas Southwestern Medical School, 5323 Harry Hines Boulevard, Dallas, TX 75390, USA

FEATURES Location/Qualifiers
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/mol_type="genomic DNA"
/strain="N2M2410"
/db_xref="taxon:10090"
/chromosome="12"
/cell_line="ZB9D4"
/cell_type="spleen plasma B-cell hybridoma"
/rearranged
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/product="ANA immunoglobulin heavy chain"
CDS <1. .>489
/note="lupus; anti-DNA; glomerulonephritis"
/codon_start=1
/product="ANA immunoglobulin heavy chain"
/protein_id="AAR90996.1"
/db_xref="GI:40794885"

/translation="VQLQQSGPGLVQPSQSL SITCTVSGFSLTSYGIHWVRQSPGKGL
EWLGVIWSGGSTDYNAPFISRLSISKDNSKSQVFFKMNSLQADDTAIYYCARNFPYGN
FDYWGGQGTALT VSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNSG
SCS"

ORIGIN

Alignment Scores:

Pred. No.:	5.19e-54	Length:	489
Score:	503.00	Matches:	94
Percent Similarity:	88.98%	Conservative:	11
Best Local Similarity:	79.66%	Mismatches:	11
Query Match:	78.84%	Indels:	2
DB:	10	Gaps:	1

US-10-631-258-13 (1-118) x AY436968 (1-489)

Qy	1	Va	Lys	Leu	Gln	Glu	Ser	Gly	Pro	Gly	Leu	Val	Gln	Pro	Ser	Gln	Ser	Leu	Ser	Ile	Thr	20
					:	:	:					:	:									
Db	1	GTGCAGCTGCAGCAGTCAGGACCTGGCCTAGTGCAGCCCTCACAGAGCCTGTCCATCACC	60																			
Qy	21	Cys	Thr	Val	Ser	Gly	Phe	Ser	Leu	Thr	Asp	Tyr	Gly	Val	His	Trp	Val	Arg	Gln	Ser	Pro	40
																:	:					
Db	61	TGCACAGTCTCTGGTTTCTCATTA	ACTAGCTATGGTATACACTGGGTTCGCCAGTCTCCA	120																		
Qy	41	Gly	Lys	Gly	Leu	Glu	Trp	Leu	Gly	Val	Ile	Trp	Ser	Gly	Cys	Gly	Thr	Ala	Tyr	Thr	Ala	60
Db	121	GGAAAGGGTCTGGAGTGGCTGGGAGTGATATGGAGTGGTGGGAAGCACAGACTATAATGCA	180																			

Qy	61	AlaPheIleSerArgLeuAsnIleTyrLysAspAsnSerLysAsnGlnValPhePheGlu	80
Db	181	CCTTTCATATCCAGACTGAGCATCAGCAAGGACAATTCCAAGAGCCAAGTTTCTTTAAA	240
Qy	81	MetAsnSerLeuGlnAlaAspAspThrAlaMetTyrTyrCysAlaArgArgGlySerTyr	100
Db	241	ATGAACAGTCTGCAAGCTGATGACACAGCCATATATTACTGTGCCAGA-----AATTTT	294
Qy	101	ProTyrAsnTyrPheAspValTrpGlyGlnGlyThrThrValThrValSerAla	118
Db	295	CCTTATGGTAACTTCGACTACTGGGGCCAAGGCACCGCTCTCACAGTCTCCTCA	348

us-10-631-258-13.p2n.rng

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 8, 2005, 15:43:35 ; Search time 442 seconds
(without alignments)
1580.383 Million cell updates/sec

Title: US-10-631-258-13
Perfect score: 638
Sequence: 1 VKLQESGPGLVQPSQSL SIT.....SYPYNYFDVWGQGTTVTVSA 118

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-DB=N_Geneseq_16Dec04 -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10631258_@CGN_1_1_708_@runat_07062005_122947_29491 -NCPUs=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_16Dec04:*
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5: geneseqn2001bs:*
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8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	638	100.0	354	13	ADQ98042	Adq98042 DNA encod
2	638	100.0	681	13	ADQ98068	Adq98068 Chimeric
3	638	100.0	765	13	ADQ98099	Adq98099 Chimeric
4	626	98.1	354	13	ADQ98040	Adq98040 DNA encod
5	626	98.1	681	13	ADQ98066	Adq98066 Chimeric
6	626	98.1	765	13	ADQ98097	Adq98097 Chimeric
7	621	97.3	354	13	ADQ98039	Adq98039 Cloned hy
8	621	97.3	681	13	ADQ98070	Adq98070 Chimeric
9	621	97.3	681	13	ADQ98065	Adq98065 Chimeric
10	621	97.3	765	13	ADQ98101	Adq98101 Chimeric
11	621	97.3	765	13	ADQ98096	Adq98096 Chimeric
12	618	96.9	354	13	ADQ98038	Adq98038 Native hy
13	618	96.9	354	13	ADQ98102	Adq98102 Native hy
14	618	96.9	354	13	ADQ98071	Adq98071 Native hy
15	617	96.7	354	13	ADQ98043	Adq98043 DNA encod
16	617	96.7	354	13	ADQ98041	Adq98041 DNA encod
17	617	96.7	681	13	ADQ98067	Adq98067 Chimeric
18	617	96.7	681	13	ADQ98069	Adq98069 Chimeric
19	617	96.7	765	13	ADQ98098	Adq98098 Chimeric
20	617	96.7	765	13	ADQ98100	Adq98100 Chimeric
21	499	78.2	810	2	AAT27010	Aat27010 Intracell
22	498.5	78.1	348	12	ADQ91073	Adq91073 Anti EpCA
23	498.5	78.1	1479	12	ADQ91081	Adq91081 Antibody
24	498.5	78.1	1479	12	ADQ91105	Adq91105 Antibody
25	498.5	78.1	1479	12	ADQ91079	Adq91079 Bispecifi
26	498.5	78.1	1479	13	ADS99440	Ads99440 Antibody
27	498.5	78.1	1479	13	ADS99446	Ads99446 Antibody
28	498.5	78.1	1479	13	ADS99434	Ads99434 Antibody
29	498.5	78.1	1479	13	ADS99450	Ads99450 Antibody
30	498.5	78.1	1479	13	ADS99430	Ads99430 Antibody
31	498.5	78.1	1479	13	ADS99442	Ads99442 Antibody
32	498.5	78.1	1479	13	ADS99432	Ads99432 Antibody
33	498.5	78.1	1479	13	ADS99444	Ads99444 Antibody
34	498.5	78.1	1479	13	ADS99448	Ads99448 Antibody
35	498.5	78.1	1479	13	ADS99454	Ads99454 Antibody
36	497.5	78.0	1371	3	AAZ50584	Aaz50584 M79scFv-i
37	497.5	78.0	1380	13	ADR43338	Adr43338 scFv anti
38	497.5	78.0	1389	3	AAZ50585	Aaz50585 M79scFv-i
39	493.5	77.4	1479	12	ADQ91091	Adq91091 Antibody
40	490	76.8	414	5	AAF58728	Aaf58728 Murine mi
41	490	76.8	414	12	ADO47748	Ado47748 Mouse mik
42	488.5	76.6	342	6	AAD28602	Aad28602 Escherich
43	484.5	75.9	753	12	ADG28587	Adg28587 Paramyxov
44	484.5	75.9	855	10	ACC57516	Acc57516 Costimula
45	484.5	75.9	1479	12	ADQ91089	Adq91089 Antibody

ALIGNMENTS

RESULT 1

ADQ98042

ID ADQ98042 standard; DNA; 354 BP.

XX

AC ADQ98042;

XX

DT 21-OCT-2004 (first entry)

XX

DE DNA encodes mutant murine antibody 2D12.5 variable heavy chain N87D G54C.
 XX
 KW murine; mouse; gene; ds; antigen recognition domain; in vivo imaging;
 KW cell-antibody-metal chelate complex; emission tomography;
 KW magnetic resonance imaging; lanthanide luminescence; gamma-emissions;
 KW single photon emission tomography; SPET; cancer; cytostatic;
 KW immunosuppressive; multi-functional antibody; metal chelate; mutant.
 XX
 OS Mus musculus.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
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 FT /product= "Mutant murine 2D12.5 heavy chain variable
 FT protein"
 FT /note= "Start and stop codons are absent"
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 PN WO2004065569-A2.
 XX
 PD 05-AUG-2004.
 XX
 PF 23-JAN-2004; 2004WO-US001808.
 XX
 PR 23-JAN-2003; 2003US-00350555.
 PR 22-JUL-2003; 2003US-00625047.
 PR 31-JUL-2003; 2003US-00631258.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Meares C, Corneillie T;
 XX
 DR WPI; 2004-580725/56.
 DR P-PSDB; ADQ98036.
 XX
 PT Novel mutant antibody comprising reactive site not present in wild-type
 PT of antibody and antigen recognition domain that recognizes macrocyclic
 PT metal chelate having four nitrogen atoms, useful for treating cancer or
 PT autoimmune diseases.
 XX
 PS Claim 40; SEQ ID NO 19; 208pp; English.
 XX
 CC This invention relates to multi-functional antibodies that recognise
 CC chelating agents and metal chelates, particularly macrocyclic metal
 CC chelates. Specifically, it refers to an antibody that comprises a metal
 CC chelate bound to an antigen recognition domain, where the metal chelate
 CC has a reactive functional group of complementary reactivity to the
 CC reactive site of the antibody. This reactive site is the side chain of a
 CC naturally occurring amino acid e.g. the -SH group side chain of a
 CC cysteine residue (not present in the wild type) which can be used to form
 CC a covalent bond between the reactive site of the antibody and the
 CC reactive functional group of the metal chelate. The present invention
 CC describes using these antibodies for in vivo imaging where the antibody
 CC comprises a targeting moiety that binds specifically to a cell via a cell
 CC surface receptor or antigen thus forming a cell-mutant antibody complex.
 CC On addition of the metal chelate, a cell-antibody-metal chelate complex
 CC is formed that can be detected using emission tomography, magnetic
 CC resonance imaging, lanthanide luminescence, gamma-emissions or single
 CC photon emission tomography (SPET). As such, this method is useful for
 CC treating a subject with cancer and pharmaceutical compositions exhibit
 CC cytostatic and immunosuppressive activities. This polynucleotide sequence
 CC is the DNA encoding a mutant murine antibody 2D12.5 variable heavy chain

us-10-631-258-13.p2n.rng

CC protein of the invention.

XX

SQ Sequence 354 BP; 83 A; 90 C; 96 G; 85 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	5e-63	Length:	354
Score:	638.00	Matches:	118
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	13	Gaps:	0

US-10-631-258-13 (1-118) x ADQ98042 (1-354)

Qy	1	VaLLysLeuGlnGluSerGlyProGlyLeuValGlnProSerGlnSerLeuSerIleThr	20
Db	1	GTGAAGCTGCAGGAGTCTGGGCCTGGCCTAGTGCAGCCCTCACAGAGCCTGTCCATCACC	60
Qy	21	CysThrValSerGlyPheSerLeuThrAspTyrGlyValHisTrpValArgGlnSerPro	40
Db	61	TGCACGGTCTCTGGTTTCTCATTAAGTACTATGGTGTACACTGGGTTCGCCAGTCTCCA	120
Qy	41	GlyLysGlyLeuGluTrpLeuGlyValIleTrpSerGlyCysGlyThrAlaTyrThrAla	60
Db	121	GGAAAGGGTCTGGAATGGCTGGGAGTGATATGGAGTGGTTGTGGCACGGCCTATACTGCG	180
Qy	61	AlaPheIleSerArgLeuAsnIleTyrLysAspAsnSerLysAsnGlnValPhePheGlu	80
Db	181	GCGTTCATATCCAGACTGAACATCTACAAGGACAATTCCAAGAACCAAGTTTTCTTTGAA	240
Qy	81	MetAsnSerLeuGlnAlaAspAspThrAlaMetTyrTyrCysAlaArgArgGlySerTyr	100
Db	241	ATGAACAGTCTGCAAGCTGATGACACAGCCATGTATTACTGTGCCAGAAGGGGTAGCTAC	300
Qy	101	ProTyrAsnTyrPheAspValTrpGlyGlnGlyThrThrValThrValSerAla	118
Db	301	CCTTACAACACTTTCGATGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCGCA	354

RESULT 2

ADQ98068

ID ADQ98068 standard; DNA; 681 BP.

XX

AC ADQ98068;

XX

DT 21-OCT-2004 (first entry)

XX

DE Chimeric murine N87D G54C 2D12.5 VH antibody fused to human TTCH DNA.

XX

KW murine; mouse; gene; ds; chimeric; human; TTCH; tetanus toxin;

KW magnetic resonance imaging; lanthanide luminescence; gamma-emissions;

KW single photon emission tomography; SPET; cancer; cytostatic;

KW immunosuppressive; multi-functional antibody; metal chelate;

KW antigen recognition domain; in vivo imaging;

KW cell-antibody-metal chelate complex; emission tomography; mutant.

XX

OS Mus musculus.

OS Homo sapiens.

OS Chimeric.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT CDS 1. .681

FT /*tag= a


```

us-10-631-258-13.p2n.rng
FT      /partial
FT      /product= "Chimeric mutant murine 2D12.5 human anti-
FT      tetanus toxin antibody protein"
FT      /note= "Start and stop codons are absent"
XX
PN      WO2004065569-A2.
XX
PD      05-AUG-2004.
XX
PF      23-JAN-2004; 2004WO-US001808.
XX
PR      23-JAN-2003; 2003US-00350555.
PR      22-JUL-2003; 2003US-00625047.
PR      31-JUL-2003; 2003US-00631258.
XX
PA      (REGC ) UNIV CALIFORNIA.
XX
PI      Meares C, Corneillie T;
XX
DR      WPI; 2004-580725/56.
DR      P-PSDB; ADQ98061.
XX
PT      Novel mutant antibody comprising reactive site not present in wild-type
PT      of antibody and antigen recognition domain that recognizes macrocyclic
PT      metal chelate having four nitrogen atoms, useful for treating cancer or
PT      autoimmune diseases.
XX
PS      Claim 40; SEQ ID NO 45; 208pp; English.
XX
CC      This invention relates to multi-functional antibodies that recognise
CC      chelating agents and metal chelates, particularly macrocyclic metal
CC      chelates. Specifically, it refers to an antibody that comprises a metal
CC      chelate bound to an antigen recognition domain, where the metal chelate
CC      has a reactive functional group of complementary reactivity to the
CC      reactive site of the antibody. This reactive site is the side chain of a
CC      naturally occurring amino acid e.g. the -SH group side chain of a
CC      cysteine residue (not present in the wild type) which can be used to form
CC      a covalent bond between the reactive site of the antibody and the
CC      reactive functional group of the metal chelate. The present invention
CC      describes using these antibodies for in vivo imaging where the antibody
CC      comprises a targeting moiety that binds specifically to a cell via a cell
CC      surface receptor or antigen thus forming a cell-mutant antibody complex.
CC      On addition of the metal chelate, a cell-antibody-metal chelate complex
CC      is formed that can be detected using emission tomography, magnetic
CC      resonance imaging, lanthanide luminescence, gamma-emissions or single
CC      photon emission tomography (SPET). As such, this method is useful for
CC      treating a subject with cancer and pharmaceutical compositions exhibit
CC      cytostatic and immunosuppressive activities. This polynucleotide sequence
CC      is the DNA encoding a chimeric mutant N87D G54C murine antibody 2D12.5
CC      variable heavy chain protein fused to the human anti-tetanus toxin
CC      antibody CH1 heavy chain constant region of the invention.
XX
SQ      Sequence 681 BP; 155 A; 208 C; 177 G; 141 T; 0 U; 0 Other;

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Alignment Scores:

Pred. No.:	1.13e-62	Length:	681
Score:	638.00	Matches:	118
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	13	Gaps:	0

US-10-631-258-13 (1-118) x ADQ98068 (1-681)

us-10-631-258-13.p2n.rng

Qy	1	ValLysLeuGlnGluSerGlyProGlyLeuValGlnProSerGlnSerLeuSerIleThr	20
Db	7	GTGAAGCTGCAGGAGTCTGGGCCTGGCCTAGTGCAGCCCTCACAGAGCCTGTCCATCACC	66
Qy	21	CysThrValSerGlyPheSerLeuThrAspTyrGlyValHisTrpValArgGlnSerPro	40
Db	67	TGCACGGTCTCTGGTTTCTCATTAAGTACTGACTATGGTGTACACTGGGTTCGCCAGTCTCCA	126
Qy	41	GlyLysGlyLeuGluTrpLeuGlyValIleTrpSerGlyCysGlyThrAlaTyrThrAla	60
Db	127	GGAAAGGGTCTGGAATGGCTGGGAGTGATATGGAGTGGTTGTGGCACGGCCTATACTGCG	186
Qy	61	AlaPheIleSerArgLeuAsnIleTyrLysAspAsnSerLysAsnGlnValPhePheGlu	80
Db	187	GCGTTCATATCCAGACTGAACATCTACAAGGACAATTCCAAGAACCAAGTTTTCTTTGAA	246
Qy	81	MetAsnSerLeuGlnAlaAspAspThrAlaMetTyrTyrCysAlaArgArgGlySerTyr	100
Db	247	ATGAACAGTCTGCAAGCTGATGACACAGCCATGTATTACTGTGCCAGAAGGGGTAGCTAC	306
Qy	101	ProTyrAsnTyrPheAspValTrpGlyGlnGlyThrThrValThrValSerAla	118
Db	307	CCTTACAACACTTTCGATGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCGCA	360

RESULT 3

ADQ98099

ID ADQ98099 standard; DNA; 765 BP.

XX

AC ADQ98099;

XX

DT 21-OCT-2004 (first entry)

XX

DE Chimeric 2dVH-TTCH DNA with tag encoding N87D/G54C mutations SeqID 76.

XX

KW murine; mouse; gene; ds; chimeric; human; TTCH; tetanus toxin;
KW magnetic resonance imaging; lanthanide luminescence; gamma-emissions;
KW single photon emission tomography; SPET; cancer; cytostatic;
KW immunosuppressive; multi-functional antibody; metal chelate;
KW antigen recognition domain; in vivo imaging;
KW cell-antibody-metal chelate complex; emission tomography; V5 epitope;
KW His tag; mutant.

XX

OS Mus musculus.

OS Homo sapiens.

OS Chimeric.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT CDS

1. .765

FT

/*tag= a

FT

/partial

FT

/product= "Chimeric murine 2D12.5 human anti-tetanus

FT

toxin TTCH antibody protein with V5 epitope and His tag"

FT

/note= "Start codon is absent"

XX

PN WO2004065569-A2.

XX

PD 05-AUG-2004.

XX

PF 23-JAN-2004; 2004WO-US001808.

XX

PR 23-JAN-2003; 2003US-00350555.

PR 22-JUL-2003; 2003US-00625047.
 PR 31-JUL-2003; 2003US-00631258.

XX
 PA (REGC) UNIV CALIFORNIA.

XX
 PI Meares C, Corneillie T;

XX
 DR WPI; 2004-580725/56.
 DR P-PSDB; ADQ98106.

XX
 PT Novel mutant antibody comprising reactive site not present in wild-type
 PT of antibody and antigen recognition domain that recognizes macrocyclic
 PT metal chelate having four nitrogen atoms, useful for treating cancer or
 PT autoimmune diseases.

XX
 PS Claim 40; SEQ ID NO 76; 208pp; English.

XX
 CC This invention relates to multi-functional antibodies that recognise
 CC chelating agents and metal chelates, particularly macrocyclic metal
 CC chelates. Specifically, it refers to an antibody that comprises a metal
 CC chelate bound to an antigen recognition domain, where the metal chelate
 CC has a reactive functional group of complementary reactivity to the
 CC reactive site of the antibody. This reactive site is the side chain of a
 CC naturally occurring amino acid e.g. the -SH group side chain of a
 CC cysteine residue (not present in the wild type) which can be used to form
 CC a covalent bond between the reactive site of the antibody and the
 CC reactive functional group of the metal chelate. The present invention
 CC describes using these antibodies for in vivo imaging where the antibody
 CC comprises a targeting moiety that binds specifically to a cell via a cell
 CC surface receptor or antigen thus forming a cell-mutant antibody complex.
 CC On addition of the metal chelate, a cell-antibody-metal chelate complex
 CC is formed that can be detected using emission tomography, magnetic
 CC resonance imaging, lanthanide luminescence, gamma-emissions or single
 CC photon emission tomography (SPET). As such, this method is useful for
 CC treating a subject with cancer and pharmaceutical compositions exhibit
 CC cytostatic and immunosuppressive activities. This polynucleotide is the
 CC mutant DNA sequence encoding a chimeric murine antibody 2D12.5 variable
 CC heavy chain protein fused to the human anti-tetanus toxin antibody CH1
 CC heavy chain constant region (2dVH-TTCH) with N87D and G54C mutations and
 CC a V5 epitope with (His)₆ tag, given in an exemplification of the
 CC invention.

XX
 SQ Sequence 765 BP; 172 A; 239 C; 192 G; 162 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.31e-62	Length:	765
Score:	638.00	Matches:	118
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	13	Gaps:	0

US-10-631-258-13 (1-118) x ADQ98099 (1-765)

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Qy	21	Cys	Thr	Val	Ser	Gly	Phe	Ser	Leu	Thr	Asp	Tyr	Gly	Val	His	Trp	Val	Arg	Gln	Ser	Pro	40
Db	67	TG	CA	CG	GT	CT	CT	GG	TTT	CT	CA	TTA	ACT	GA	CT	AT	GG	TG	TAC	ACT	GG	126
Qy	41	Gly	Lys	Gly	Leu	Glu	Trp	Leu	Gly	Val	Ile	Trp	Ser	Gly	Cys	Gly	Thr	Ala	Tyr	Thr	Ala	60

us-10-631-258-13.p2n.rng

Db	127	GGAAAGGGTCTGGAATGGCTGGGAGTGATATGGAGTGTTGTGGCACGGCCTATACTGCG	186
Qy	61	AlaPheIleSerArgLeuAsnIleTyrLysAspAsnSerLysAsnGlnValPhePheGlu	80
Db	187	GCGTTCATATCCAGACTGAACATCTACAAGGACAATTCCAAGAACCAAGTTTTCTTTGAA	246
Qy	81	MetAsnSerLeuGlnAlaAspAspThrAlaMetTyrTyrCysAlaArgArgGlySerTyr	100
Db	247	ATGAACAGTCTGCAAGCTGATGACACAGCCATGTATTACTGTGCCAGAAGGGGTAGCTAC	306
Qy	101	ProTyrAsnTyrPheAspValTrpGlyGlnGlyThrThrValThrValSerAla	118
Db	307	CCTTACAACACTTTCGATGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCGCA	360

RESULT 4
ADQ98040

ID ADQ98040 standard; DNA; 354 BP.

XX

AC ADQ98040;

XX

DT 21-OCT-2004 (first entry)

XX

DE DNA encoding the mutant murine antibody 2D12.5 variable heavy chain N87D.

XX

KW murine; mouse; gene; ds; antigen recognition domain; in vivo imaging;

KW cell-antibody-metal chelate complex; emission tomography;

KW magnetic resonance imaging; lanthanide luminescence; gamma-emissions;

KW single photon emission tomography; SPET; cancer; cytostatic;

KW immunosuppressive; multi-functional antibody; metal chelate; mutant.

XX

OS Mus musculus.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT CDS 1. .354

FT /*tag= a

FT /partial

FT /product= "Mutant murine 2D12.5 heavy chain variable protein"

FT /note= "Start and stop codons are absent"

XX

PN WO2004065569-A2.

XX

PD 05-AUG-2004.

XX

PF 23-JAN-2004; 2004WO-US001808.

XX

PR 23-JAN-2003; 2003US-00350555.

PR 22-JUL-2003; 2003US-00625047.

PR 31-JUL-2003; 2003US-00631258.

XX

PA (REGC) UNIV CALIFORNIA.

XX

PI Meares C, Corneillie T;

XX

DR WPI; 2004-580725/56.

DR P-PSDB; ADQ98034.

XX

PT Novel mutant antibody comprising reactive site not present in wild-type
PT of antibody and antigen recognition domain that recognizes macrocyclic
PT metal chelate having four nitrogen atoms, useful for treating cancer or
PT autoimmune diseases.

XX

PS Claim 40; SEQ ID NO 17; 208pp; English.

XX

CC This invention relates to multi-functional antibodies that recognise
 CC chelating agents and metal chelates, particularly macrocyclic metal
 CC chelates. Specifically, it refers to an antibody that comprises a metal
 CC chelate bound to an antigen recognition domain, where the metal chelate
 CC has a reactive functional group of complementary reactivity to the
 CC reactive site of the antibody. This reactive site is the side chain of a
 CC naturally occurring amino acid e.g. the -SH group side chain of a
 CC cysteine residue (not present in the wild type) which can be used to form
 CC a covalent bond between the reactive site of the antibody and the
 CC reactive functional group of the metal chelate. The present invention
 CC describes using these antibodies for in vivo imaging where the antibody
 CC comprises a targeting moiety that binds specifically to a cell via a cell
 CC surface receptor or antigen thus forming a cell-mutant antibody complex.
 CC On addition of the metal chelate, a cell-antibody-metal chelate complex
 CC is formed that can be detected using emission tomography, magnetic
 CC resonance imaging, lanthanide luminescence, gamma-emissions or single
 CC photon emission tomography (SPET). As such, this method is useful for
 CC treating a subject with cancer and pharmaceutical compositions exhibit
 CC cytostatic and immunosuppressive activities. This polynucleotide sequence
 CC is the DNA encoding a mutant murine antibody 2D12.5 variable heavy chain
 CC protein of the invention.

XX

SQ Sequence 354 BP; 85 A; 90 C; 96 G; 83 T; 0 U; 0 other;

Alignment Scores:

Pred. No.:	1.14e-61	Length:	354
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Percent Similarity:	99.15%	Conservative:	0
Best Local Similarity:	99.15%	Mismatches:	1
Query Match:	98.12%	Indels:	0
DB:	13	Gaps:	0

US-10-631-258-13 (1-118) x ADQ98040 (1-354)

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Qy	21	CysThrValSerGlyPheSerLeuThrAspTyrGlyValHisTrpValArgGlnSerPro	40
Db	61	TGCACGGTCTCTGTTTCTCATTAAGTACTATGGTGTACACTGGGTTCGCCAGTCTCCA	120
Qy	41	GlyLysGlyLeuGluTrpLeuGlyValIleTrpSerGlyCysGlyThrAlaTyrThrAla	60
Db	121	GGAAAGGGTCTGGAATGGCTGGGAGTGATATGGAGTGGTGGAGGCACGGCCTATACTGCG	180
Qy	61	AlaPheIleSerArgLeuAsnIleTyrLysAspAsnSerLysAsnGlnValPhePheGlu	80
Db	181	GCGTTCATATCCAGACTGAACATCTACAAGGACAATTCCAAGAACCAAGTTTTCTTTGAA	240
Qy	81	MetAsnSerLeuGlnAlaAspAspThrAlaMetTyrTyrCysAlaArgArgGlySerTyr	100
Db	241	ATGAACAGTCTGCAAGCTGATGACACAGCCATGTATTACTGTGCCAGAAGGGGTAGCTAC	300
Qy	101	ProTyrAsnTyrPheAspValTrpGlyGlnGlyThrThrValThrValSerAla	118
Db	301	CCTTACAACACTTTCGATGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCGCA	354

RESULT 5
 ADQ98066

ID ADQ98066 standard; DNA; 681 BP.
XX
AC ADQ98066;
XX
DT 21-OCT-2004 (first entry)
XX
DE Chimeric murine N87D 2D12.5 VH antibody fused to human TTCH DNA.
XX
KW murine; mouse; gene; ds; chimeric; human; TTCH; tetanus toxin;
KW magnetic resonance imaging; lanthanide luminescence; gamma-emissions;
KW single photon emission tomography; SPET; cancer; cytostatic;
KW immunosuppressive; multi-functional antibody; metal chelate;
KW antigen recognition domain; in vivo imaging;
KW cell-antibody-metal chelate complex; emission tomography; mutant.
XX
OS Mus musculus.
OS Homo sapiens.
OS Chimeric.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 1. .681
FT /*tag= a
FT /partial
FT /product= "Chimeric mutant murine 2D12.5 human anti-
FT tetanus toxin antibody protein"
FT /note= "Start and stop codons are absent"
XX
PN WO2004065569-A2.
XX
PD 05-AUG-2004.
XX
PF 23-JAN-2004; 2004WO-US001808.
XX
PR 23-JAN-2003; 2003US-00350555.
PR 22-JUL-2003; 2003US-00625047.
PR 31-JUL-2003; 2003US-00631258.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Meares C, Corneillie T;
XX
DR WPI; 2004-580725/56.
DR P-PSDB; ADQ98059.
XX
PT Novel mutant antibody comprising reactive site not present in wild-type
PT of antibody and antigen recognition domain that recognizes macrocyclic
PT metal chelate having four nitrogen atoms, useful for treating cancer or
PT autoimmune diseases.
XX
PS Claim 40; SEQ ID NO 43; 208pp; English.
XX
CC This invention relates to multi-functional antibodies that recognise
CC chelating agents and metal chelates, particularly macrocyclic metal
CC chelates. Specifically, it refers to an antibody that comprises a metal
CC chelate bound to an antigen recognition domain, where the metal chelate
CC has a reactive functional group of complementary reactivity to the
CC reactive site of the antibody. This reactive site is the side chain of a
CC naturally occurring amino acid e.g. the -SH group side chain of a
CC cysteine residue (not present in the wild type) which can be used to form
CC a covalent bond between the reactive site of the antibody and the
CC reactive functional group of the metal chelate. The present invention
CC describes using these antibodies for in vivo imaging where the antibody

us-10-631-258-13.p2n.rng

CC comprises a targeting moiety that binds specifically to a cell via a cell
CC surface receptor or antigen thus forming a cell-mutant antibody complex.
CC On addition of the metal chelate, a cell-antibody-metal chelate complex
CC is formed that can be detected using emission tomography, magnetic
CC resonance imaging, lanthanide luminescence, gamma-emissions or single
CC photon emission tomography (SPET). As such, this method is useful for
CC treating a subject with cancer and pharmaceutical compositions exhibit
CC cytostatic and immunosuppressive activities. This polynucleotide sequence
CC is the DNA encoding a chimeric mutant N87D murine antibody 2D12.5
CC variable heavy chain protein fused to the human anti-tetanus toxin
CC antibody CH1 heavy chain constant region of the invention.

XX

SQ Sequence 681 BP; 157 A; 208 C; 177 G; 139 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2.58e-61	Length:	681
Score:	626.00	Matches:	117
Percent Similarity:	99.15%	Conservative:	0
Best Local Similarity:	99.15%	Mismatches:	1
Query Match:	98.12%	Indels:	0
DB:	13	Gaps:	0

US-10-631-258-13 (1-118) x ADQ98066 (1-681)

Qy	1	VaLLysLeuGlnGluSerGlyProGlyLeuValGlnProSerGlnSerLeuSerIleThr	20
Db	7	GTGAAGCTGCAGGAGTCTGGACCTGGCCTAGTGCAGCCCTCACAGAGCCTGTCCATCACC	66
Qy	21	CysThrValSerGlyPheSerLeuThrAspTyrGlyValHisTrpValArgGlnSerPro	40
Db	67	TGCACGGTCTCTGGTTTCTCATTAAGTACTATGGTGTACACTGGGTTCGCCAGTCTCCA	126
Qy	41	GlyLysGlyLeuGluTrpLeuGlyValIleTrpSerGlyCysGlyThrAlaTyrThrAla	60
Db	127	GGAAAGGGTCTGGAATGGCTGGGAGTGATATGGAGTGGTGGAGGCACGGCCTATACTGCG	186
Qy	61	AlaPheIleSerArgLeuAsnIleTyrLysAspAsnSerLysAsnGlnValPhePheGlu	80
Db	187	GCGTTCATATCCAGACTGAACATCTACAAGGACAATTCCAAGAACCAAGTTTTCTTTGAA	246
Qy	81	MetAsnSerLeuGlnAlaAspAspThrAlaMetTyrTyrCysAlaArgArgGlySerTyr	100
Db	247	ATGAACAGTCTGCAAGCTGATGACACAGCCATGTATTACTGTGCCAGAAGGGGTAGCTAC	306
Qy	101	ProTyrAsnTyrPheAspValTrpGlyGlnGlyThrThrValThrValSerAla	118
Db	307	CCTTACAACACTTTCGATGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCGCA	360

us-10-631-258-13.p2n.rnpb

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

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Listing first 45 summaries

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11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*

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                                us-10-631-258-13.p2n.rnpb
18:  /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
19:  /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
20:  /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq:*
21:  /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq:*
22:  /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
23:  /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
24:  /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
25:  /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
26:  /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	638	100.0	354	19	US-10-625-047-19	Sequence 19, Appl
2	638	100.0	354	21	US-10-631-258-19	Sequence 19, Appl
3	638	100.0	354	21	US-10-854-735-19	Sequence 19, Appl
4	638	100.0	354	21	US-10-835-533-19	Sequence 19, Appl
5	638	100.0	681	19	US-10-625-047-45	Sequence 45, Appl
6	638	100.0	681	21	US-10-631-258-45	Sequence 45, Appl
7	626	98.1	354	19	US-10-625-047-17	Sequence 17, Appl
8	626	98.1	354	21	US-10-631-258-17	Sequence 17, Appl
9	626	98.1	354	21	US-10-854-735-17	Sequence 17, Appl
10	626	98.1	354	21	US-10-835-533-17	Sequence 17, Appl
11	626	98.1	681	19	US-10-625-047-43	Sequence 43, Appl
12	626	98.1	681	21	US-10-631-258-43	Sequence 43, Appl
13	621	97.3	354	19	US-10-625-047-16	Sequence 16, Appl
14	621	97.3	354	21	US-10-631-258-16	Sequence 16, Appl
15	621	97.3	354	21	US-10-854-735-16	Sequence 16, Appl
16	621	97.3	354	21	US-10-835-533-16	Sequence 16, Appl
17	621	97.3	681	19	US-10-625-047-42	Sequence 42, Appl
18	621	97.3	681	19	US-10-625-047-47	Sequence 47, Appl
19	621	97.3	681	21	US-10-631-258-42	Sequence 42, Appl
20	621	97.3	681	21	US-10-631-258-47	Sequence 47, Appl
21	618	96.9	354	19	US-10-625-047-15	Sequence 15, Appl
22	618	96.9	354	19	US-10-625-047-48	Sequence 48, Appl
23	618	96.9	354	21	US-10-631-258-15	Sequence 15, Appl
24	618	96.9	354	21	US-10-631-258-48	Sequence 48, Appl
25	618	96.9	354	21	US-10-854-735-15	Sequence 15, Appl
26	618	96.9	354	21	US-10-835-533-15	Sequence 15, Appl
27	617	96.7	354	19	US-10-625-047-18	Sequence 18, Appl
28	617	96.7	354	19	US-10-625-047-20	Sequence 20, Appl
29	617	96.7	354	21	US-10-631-258-18	Sequence 18, Appl
30	617	96.7	354	21	US-10-631-258-20	Sequence 20, Appl
31	617	96.7	354	21	US-10-854-735-18	Sequence 18, Appl
32	617	96.7	354	21	US-10-854-735-20	Sequence 20, Appl
33	617	96.7	354	21	US-10-835-533-18	Sequence 18, Appl
34	617	96.7	354	21	US-10-835-533-20	Sequence 20, Appl
35	617	96.7	681	19	US-10-625-047-44	Sequence 44, Appl
36	617	96.7	681	19	US-10-625-047-46	Sequence 46, Appl
37	617	96.7	681	21	US-10-631-258-44	Sequence 44, Appl
38	617	96.7	681	21	US-10-631-258-46	Sequence 46, Appl
39	498.5	78.1	348	19	US-10-682-845-54	Sequence 54, Appl
40	498.5	78.1	1479	19	US-10-682-845-60	Sequence 60, Appl
41	498.5	78.1	1479	19	US-10-682-845-62	Sequence 62, Appl
42	498.5	78.1	1479	19	US-10-682-845-64	Sequence 64, Appl
43	498.5	78.1	1479	19	US-10-682-845-66	Sequence 66, Appl
44	498.5	78.1	1479	19	US-10-682-845-68	Sequence 68, Appl

ALIGNMENTS

RESULT 1

US-10-625-047-19

; Sequence 19, Application US/10625047

; Publication No. US20040198962A1

; GENERAL INFORMATION:

; APPLICANT: Meares, Claude

; APPLICANT: Corneillie, Todd

; APPLICANT: The Regents of the University of California

; TITLE OF INVENTION: Multi-Functional Antibodies

; FILE REFERENCE: 023070-130910US

; CURRENT APPLICATION NUMBER: US/10/625,047

; CURRENT FILING DATE: 2003-07-22

; PRIOR APPLICATION NUMBER: US 10/350,555

; PRIOR FILING DATE: 2003-01-23

; NUMBER OF SEQ ID NOS: 72

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 19

; LENGTH: 354

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:N87D G54C

; OTHER INFORMATION: cloned mutant murine 2D12.5 heavy chain variable

; OTHER INFORMATION: region (VH)

US-10-625-047-19

Alignment Scores:

Pred. No.:	3.33e-77	Length:	354
Score:	638.00	Matches:	118
Percent similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	19	Gaps:	0

US-10-631-258-13 (1-118) x US-10-625-047-19 (1-354)

Qy	1	ValLysLeuGlnGluSerGlyProGlyLeuValGlnProSerGlnSerLeuSerIleThr	20
Db	1	GTGAAGCTGCAGGAGTCTGGGCCTGGCCTAGTGCAGCCCTCACAGAGCCTGTCCATCACC	60
Qy	21	CysThrValSerGlyPheSerLeuThrAspTyrGlyValHisTrpValArgGlnSerPro	40
Db	61	TGCACGGTCTCTGGTTTCTCATTAAGTACTGACTATGGTGTACACTGGGTTCGCCAGTCTCCA	120
Qy	41	GlyLysGlyLeuGluTrpLeuGlyValIleTrpSerGlyCysGlyThrAlaTyrThrAla	60
Db	121	GGAAAGGGTCTGGAATGGCTGGGAGTGATATGGAGTGGTTGTGGCACGGCCTATACTGCG	180
Qy	61	AlaPheIleSerArgLeuAsnIleTyrLysAspAsnSerLysAsnGlnValPhePheGlu	80
Db	181	GCGTTCATATCCAGACTGAACATCTACAAGGACAATTCCAAGAACCAAGTTTCTTTGAA	240
Qy	81	MetAsnSerLeuGlnAlaAspAspThrAlaMetTyrTyrCysAlaArgArgGlySerTyr	100
Db	241	ATGAACAGTCTGCAAGCTGATGACACAGCCATGTATTACTGTGCCAGAAGGGGTAGCTAC	300
Qy	101	ProTyrAsnTyrPheAspValTrpGlyGlnGlyThrThrValThrValSerAla	118

Db 301 CCTTACAACACTTTCGATGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCGCA 354

RESULT 2

US-10-631-258-19

; Sequence 19, Application US/10631258

; Publication No. US20050026263A1

; GENERAL INFORMATION:

; APPLICANT: Meares, Claude

; APPLICANT: Corneillie, Todd

; APPLICANT: The Regents of the University of California

; TITLE OF INVENTION: Multi-Functional Antibodies

; FILE REFERENCE: 023070-130920US

; CURRENT APPLICATION NUMBER: US/10/631,258

; CURRENT FILING DATE: 2003-07-31

; PRIOR APPLICATION NUMBER: US 10/350,555

; PRIOR FILING DATE: 2003-01-23

; PRIOR APPLICATION NUMBER: US 10/625,047

; PRIOR FILING DATE: 2003-07-22

; NUMBER OF SEQ ID NOS: 72

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 19

; LENGTH: 354

; TYPE: DNA

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:N87D G54C

; OTHER INFORMATION: cloned mutant murine 2D12.5 heavy chain variable

; OTHER INFORMATION: region (VH)

US-10-631-258-19

Alignment Scores:

Pred. No.:	3.33e-77	Length:	354
Score:	638.00	Matches:	118
Percent similarity:	100.00%	Conservative:	0
Best Local similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	21	Gaps:	0

US-10-631-258-13 (1-118) x US-10-631-258-19 (1-354)

Qy	1	ValLysLeuGlnGluSerGlyProGlyLeuValGlnProSerGlnSerLeuSerIleThr	20
Db	1	GTGAAGCTGCAGGAGTCTGGGCCTGGCCTAGTGCAGCCCTCACAGAGCCTGTCCATCACC	60
Qy	21	CysThrValSerGlyPheSerLeuThrAspTyrGlyValHisTrpValArgGlnSerPro	40
Db	61	TGCACGGTCTCTGGTTTCTCATTAAGTACTATGGTGTACACTGGGTTCGCCAGTCTCCA	120
Qy	41	GlyLysGlyLeuGluTrpLeuGlyValIleTrpSerGlyCysGlyThrAlaTyrThrAla	60
Db	121	GGAAAGGGTCTGGAATGGCTGGGAGTGATATGGAGTGGTTGTGGCACGGCCTATACTGCG	180
Qy	61	AlaPheIleSerArgLeuAsnIleTyrLysAspAsnSerLysAsnGlnValPhePheGlu	80
Db	181	GCGTTCATATCCAGACTGAACATCTACAAGGACAATTCCAAGAACCAAGTTTTCTTTGAA	240
Qy	81	MetAsnSerLeuGlnAlaAspAspThrAlaMetTyrTyrCysAlaArgArgGlySerTyr	100
Db	241	ATGAACAGTCTGCAAGCTGATGACACAGCCATGTATTACTGTGCCAGAAGGGGTAGCTAC	300
Qy	101	ProTyrAsnTyrPheAspValTrpGlyGlnGlyThrThrValThrValSerAla	118
Db	301	CCTTACAACACTTTCGATGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCGCA	354

RESULT 3

US-10-854-735-19

; Sequence 19, Application US/10854735

; Publication No. US20050042695A1

; GENERAL INFORMATION:

; APPLICANT: Meares, Claude F.

; APPLICANT: Lebrilla, Carlito B.

; APPLICANT: Butlin, Nathaniel G.

; APPLICANT: Cheal, Sarah M.

; APPLICANT: Corneillie, Todd M.

; APPLICANT: Lee, Susan

; APPLICANT: Whetstone, Paul A.

; APPLICANT: Young, Nicolas L.

; APPLICANT: The Regents of the University of California

; TITLE OF INVENTION: Element-Coded Affinity Tags

; FILE REFERENCE: 023070-136830US

; CURRENT APPLICATION NUMBER: US/10/854,735

; CURRENT FILING DATE: 2004-05-24

; PRIOR APPLICATION NUMBER: US 60/466,529

; PRIOR FILING DATE: 2003-04-28

; PRIOR APPLICATION NUMBER: US 60/495,449

; PRIOR FILING DATE: 2003-08-15

; PRIOR APPLICATION NUMBER: US 10/835,533

; PRIOR FILING DATE: 2004-04-28

; NUMBER OF SEQ ID NOS: 58

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 19

; LENGTH: 354

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial sequence:mouse

; OTHER INFORMATION: monoclonal antibody 2D12.5 heavy chain variable

; OTHER INFORMATION: domain (V-H) N87D_G54C cloned sequence

US-10-854-735-19

Alignment Scores:

Pred. No.: 3.33e-77 Length: 354

Score: 638.00 Matches: 118

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 21 Gaps: 0

US-10-631-258-13 (1-118) x US-10-854-735-19 (1-354)

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Qy      1 ValLysLeuGlnGluSerGlyProGlyLeuValGlnProSerGlnSerLeuSerIleThr 20
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Db      1 GTGAAGCTGCAGGAGTCTGGGCCTGGCCTAGTGCAGCCCTCACAGAGCCTGTCCATCACC 60

Qy     21 CysThrValSerGlyPheSerLeuThrAspTyrGlyValHisTrpValArgGlnSerPro 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TGCACGGTCTCTGGTTTCTCATTAAGTACTGACTATGGTGTACACTGGGTTCGCCAGTCTCCA 120

Qy     41 GlyLysGlyLeuGluTrpLeuGlyValIleTrpSerGlyCysGlyThrAlaTyrThrAla 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GGAAAGGGTCTGGAATGGCTGGGAGTGATATGGAGTGGTTGTGGCACGGCCTATACTGCG 180

Qy     61 AlaPheIleSerArgLeuAsnIleTyrLysAspAsnSerLysAsnGlnValPhePheGlu 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GCGTTCATATCCAGACTGAACATCTACAAGGACAATTCCAAGAACCAAGTTTTCTTTGAA 240

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                                us-10-631-258-13.p2n.rnpb
Qy      81 MetAsnSerLeuGlnAlaAspAspThrAlaMetTyrTyrCysAlaArgArgGlySerTyr 100
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Db      241 ATGAACAGTCTGCAAGCTGATGACACAGCCATGTATTACTGTGCCAGAAGGGGTAGCTAC 300

Qy      101 ProTyrAsnTyrPheAspValTrpGlyGlnGlyThrThrValThrValSerAla 118
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 CCTTACAACTACTTCGATGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCGCA 354

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RESULT 4

US-10-835-533-19

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; Sequence 19, Application US/10835533
; Publication No. US20050059100A1
; GENERAL INFORMATION:
; APPLICANT: Meares, Claude F.
; APPLICANT: Whetstone, Paul A.
; APPLICANT: Corneillie, Todd M.
; APPLICANT: Butlin, Nathaniel G.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Element-Coded Affinity Tags
; FILE REFERENCE: 023070-136820US
; CURRENT APPLICATION NUMBER: US/10/835,533
; CURRENT FILING DATE: 2004-04-28
; PRIOR APPLICATION NUMBER: US 60/466,529
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/495,449
; PRIOR FILING DATE: 2003-08-15
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 354
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:mouse
; OTHER INFORMATION: monoclonal antibody 2D12.5 heavy chain variable
; OTHER INFORMATION: domain (V-H) N87D_G54C cloned sequence
US-10-835-533-19

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Alignment Scores:

Pred. No.:	3.33e-77	Length:	354
Score:	638.00	Matches:	118
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	21	Gaps:	0

US-10-631-258-13 (1-118) x US-10-835-533-19 (1-354)

```

Qy      1 ValLysLeuGlnGluSerGlyProGlyLeuValGlnProSerGlnSerLeuSerIleThr 20
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GTGAAGCTGCAGGAGTCTGGGCCTGGCCTAGTGCAGCCCTCACAGAGCCTGTCCATCACC 60

Qy      21 CysThrValSerGlyPheSerLeuThrAspTyrGlyValHisTrpValArgGlnSerPro 40
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TGCACGGTCTCTGGTTTCTCATTAAGTACTATGGTGTACACTGGGTTCGCCAGTCTCCA 120

Qy      41 GlyLysGlyLeuGluTrpLeuGlyValIleTrpSerGlyCysGlyThrAlaTyrThrAla 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 GGAAAGGGTCTGGAATGGCTGGGAGTGATATGGAGTGGTTGTGGCACGGCCTATACTGCG 180

Qy      61 AlaPheIleSerArgLeuAsnIleTyrLysAspAsnSerLysAsnGlnValPhePheGlu 80
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 GCGTTCATATCCAGACTGAACATCTACAAGGACAATTCCAAGAACCAAGTTTCTTTGAA 240

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```

Qy      81 MetAsnSerLeuGlnAlaAspAspThrAlaMetTyrTyrCysAlaArgArgGlySerTyr 100
      |||
Db      241 ATGAACAGTCTGCAAGCTGATGACACAGCCATGTATTACTGTGCCAGAAGGGGTAGCTAC 300

Qy      101 ProTyrAsnTyrPheAspValTrpGlyGlnGlyThrThrValThrValSerAla 118
      |||
Db      301 CCTTACAACACTTCGATGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCGCA 354

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RESULT 5

US-10-625-047-45

; Sequence 45, Application US/10625047

; Publication No. US20040198962A1

; GENERAL INFORMATION:

; APPLICANT: Meares, Claude

; APPLICANT: Corneillie, Todd

; APPLICANT: The Regents of the University of California

; TITLE OF INVENTION: Multi-Functional Antibodies

; FILE REFERENCE: 023070-130910US

; CURRENT APPLICATION NUMBER: US/10/625,047

; CURRENT FILING DATE: 2003-07-22

; PRIOR APPLICATION NUMBER: US 10/350,555

; PRIOR FILING DATE: 2003-01-23

; NUMBER OF SEQ ID NOS: 72

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 45

; LENGTH: 681

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:N87D G54C

; OTHER INFORMATION: cloned mutant chimeric murine 2D12.5 heavy chain

; OTHER INFORMATION: variable region (VH) fused to human anti-tetanus

; OTHER INFORMATION: toxin antibody CH1 heavy chain constant region

; OTHER INFORMATION: (TTCH)

US-10-625-047-45

Alignment Scores:

Pred. No.:	7.99e-77	Length:	681
Score:	638.00	Matches:	118
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	19	Gaps:	0

US-10-631-258-13 (1-118) x US-10-625-047-45 (1-681)

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Qy      1 ValLysLeuGlnGluSerGlyProGlyLeuValGlnProSerGlnSerLeuSerIleThr 20
      |||
Db      7 GTGAAGCTGCAGGAGTCTGGGCCTGGCCTAGTGCAGCCCTCACAGAGCCTGTCCATCACC 66

Qy      21 CysThrValSerGlyPheSerLeuThrAspTyrGlyValHisTrpValArgGlnSerPro 40
      |||
Db      67 TGCACGGTCTCTGGTTTCTCATTAAGTACTGACTATGGTGTACACTGGGTTCGCCAGTCTCCA 126

Qy      41 GlyLysGlyLeuGluTrpLeuGlyValIleTrpSerGlyCysGlyThrAlaTyrThrAla 60
      |||
Db      127 GGAAAGGGTCTGGAATGGCTGGGAGTGATATGGAGTGGTTGTGGCACGGCCTATACTGCG 186

Qy      61 AlaPheIleSerArgLeuAsnIleTyrLysAspAsnSerLysAsnGlnValPhePheGlu 80
      |||
Db      187 GCGTTCATATCCAGACTGAACATCTACAAGGACAATTCCAAGAACCAAGTTTTCTTTGAA 246

```

```

                                us-10-631-258-13.p2n.rnpb
Qy      81 MetAsnSerLeuGlnAlaAspAspThrAlaMetTyrTyrCysAlaArgArgGlySerTyr 100
      |||
Db      247 ATGAACAGTCTGCAAGCTGATGACACAGCCATGTATTACTGTGCCAGAAGGGGTAGCTAC 306
      |||
Qy      101 ProTyrAsnTyrPheAspValTrpGlyGlnGlyThrThrValThrValSerAla 118
      |||
Db      307 CCTTACAACTACTTCGATGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCGCA 360
      |||

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RESULT 6

US-10-631-258-45

; Sequence 45, Application US/10631258

; Publication No. US20050026263A1

; GENERAL INFORMATION:

; APPLICANT: Meares, Claude

; APPLICANT: Corneillie, Todd

; APPLICANT: The Regents of the University of California

; TITLE OF INVENTION: Multi-Functional Antibodies

; FILE REFERENCE: 023070-130920US

; CURRENT APPLICATION NUMBER: US/10/631,258

; CURRENT FILING DATE: 2003-07-31

; PRIOR APPLICATION NUMBER: US 10/350,555

; PRIOR FILING DATE: 2003-01-23

; PRIOR APPLICATION NUMBER: US 10/625,047

; PRIOR FILING DATE: 2003-07-22

; NUMBER OF SEQ ID NOS: 72

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 45

; LENGTH: 681

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:N87D G54C

; OTHER INFORMATION: cloned mutant, chimeric murine 2D12.5 heavy chain

; OTHER INFORMATION: variable region (VH) fused to human anti-tetanus

; OTHER INFORMATION: toxin antibody CH1 heavy chain constant region

; OTHER INFORMATION: (TTCH)

US-10-631-258-45

Alignment Scores:

Pred. No.:	7.99e-77	Length:	681
Score:	638.00	Matches:	118
Percent similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	21	Gaps:	0

US-10-631-258-13 (1-118) x US-10-631-258-45 (1-681)

```

Qy      1 ValLysLeuGlnGluSerGlyProGlyLeuValGlnProSerGlnSerLeuSerIleThr 20
      |||
Db      7 GTGAAGCTGCAGGAGTCTGGGCCTGGCCTAGTGCAGCCCTCACAGAGCCTGTCCATCACC 66
      |||
Qy      21 CysThrValSerGlyPheSerLeuThrAspTyrGlyValHisTrpValArgGlnSerPro 40
      |||
Db      67 TGCACGGTCTCTGGTTTCTCATTAAGTACTATGGTGTACACTGGGTTCGCCAGTCTCCA 126
      |||
Qy      41 GlyLysGlyLeuGluTrpLeuGlyValIleTrpSerGlyCysGlyThrAlaTyrThrAla 60
      |||
Db      127 GGAAAGGGTCTGGAATGGCTGGGAGTGATATGGAGTGGTTGTGGCACGGCCTATACTGCG 186
      |||
Qy      61 AlaPheIleSerArgLeuAsnIleTyrLysAspAsnSerLysAsnGlnValPhePheGlu 80
      |||
Db      187 GCGTTCATATCCAGACTGAACATCTACAAGGACAATTCCAAGAACCAAGTTTTCTTTGAA 246
      |||

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Qy      81 MetAsnSerLeuGlnAlaAspAspThrAlaMetTyrTyrCysAlaArgArgGlySerTyr 100
      |||
Db      247 ATGAACAGTCTGCAAGCTGATGACACAGCCATGTATTACTGTGCCAGAAGGGGTAGCTAC 306
      |||
Qy      101 ProTyrAsnTyrPheAspValTrpGlyGlnGlyThrThrValThrValSerAla 118
      |||
Db      307 CCTTACAACACTTTCGATGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCGCA 360
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RESULT 7

US-10-625-047-17

; Sequence 17, Application US/10625047

; Publication No. US20040198962A1

; GENERAL INFORMATION:

; APPLICANT: Meares, Claude

; APPLICANT: Corneillie, Todd

; APPLICANT: The Regents of the University of California

; TITLE OF INVENTION: Multi-Functional Antibodies

; FILE REFERENCE: 023070-130910US

; CURRENT APPLICATION NUMBER: US/10/625,047

; CURRENT FILING DATE: 2003-07-22

; PRIOR APPLICATION NUMBER: US 10/350,555

; PRIOR FILING DATE: 2003-01-23

; NUMBER OF SEQ ID NOS: 72

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 17

; LENGTH: 354

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:N87D cloned

; OTHER INFORMATION: mutant murine 2D12.5 heavy chain variable region

; OTHER INFORMATION: (VH)

US-10-625-047-17

Alignment Scores:

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Query Match:	98.12%	Indels:	0
DB:	19	Gaps:	0

US-10-631-258-13 (1-118) x US-10-625-047-17 (1-354)

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Qy     21 CysThrValSerGlyPheSerLeuThrAspTyrGlyValHisTrpValArgGlnSerPro 40
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us-10-631-258-13.p2n.rnpb

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 8, 2005, 16:01:40 ; Search time 3123 Seconds
(without alignments)
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Delop 6.0 , Delext 7.0

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Total number of hits satisfying chosen parameters: 68479088

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	7	441	69.1	671	2	BF182141 601804682
	8	436.5	68.4	861	5	BU522581 AGENCOURT
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ALIGNMENTS

RESULT 1

CA577562

LOCUS CA577562 480 bp mRNA linear EST 19-NOV-2002

DEFINITION K0711B09-5N NIA Mouse Hematopoietic Stem Cell (Lin-/c-Kit-/Sca-1-)
cDNA Library (Long) Mus musculus cDNA clone NIA:K0711B09
IMAGE:30074612 5', mRNA sequence.

ACCESSION CA577562

VERSION CA577562.1 GI:25125953

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 480)

AUTHORS Piao,Y., Kargul,G.J., Dudekula,D.B., Qian,Y., Luo,A., Carter,M.G.,
Aiba,K., Taub,D., Longo,D.L., Keller,J. and Ko,M.S.H.

TITLE Systematic Analyses of NIA Mouse Hematopoietic Stem Cell
(Lin-/c-Kit-/Sca-1-) cDNA Library (Long)

JOURNAL Unpublished (2001)

COMMENT Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
Plate: K0711 row: B column: 09
Seq primer: M13 Reverse
High quality sequence stop: 480
POLYA=No.

FEATURES

source

Location/Qualifiers

1. .480

/organism="Mus musculus"

/mol_type="mRNA"

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/db_xref="niaEST:K0711B09-5N"

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/clone="NIA:K0711B09 IMAGE:30074612"

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/lab_host="DH10B"

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(Lin-/c-Kit-/Sca-1-) cDNA Library (Long)"

/note="Vector: pSPORT1 (Invitrogen); Site_1: SalI; Site_2:
NotI; Mouse cDNA project by the Laboratory of Genetics,
National Institute on Aging (NIA), Intramural Research
Program, NIH (<http://lgsun.grc.nia.nih.gov/cDNA>). This is
a long-transcript enriched cDNA library (Ref. Genome Res.
11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were
obtained from Drs. Dennis Taub, Dan Longo (National
Institute on Aging, USA), Jonathan Keller (National Cancer
Institute, USA). Double-stranded cDNAs were synthesized
with an Oligo(dT) primer [Invitrogen:
5'-pGACTAGTTCTAGATCGCGAGCGGCCCGCCCTTTTTTTTTTTTTTTT-3'] from
0.9 ug of total RNA, treated with T4 DNA polymerase, and
purified by ethanol-precipitation. The cDNAs were ligated
to Lone-linker LL-Sal4, purified by phenol/chloroform, and

separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pSPORT1 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.1 kb. The library was constructed by Yulan Piao (NIA)."

ORIGIN

Alignment Scores:

Pred. No.:	5.55e-46	Length:	480
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Percent Similarity:	88.33%	Conservative:	10
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Query Match:	76.02%	Indels:	2
DB:	6	Gaps:	0

US-10-631-258-13 (1-118) x CA577562 (1-480)

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RESULT 2

BY733751

LOCUS	BY733751	664 bp	mRNA	linear	EST 17-DEC-2002
DEFINITION	BY733751 RIKEN full-length enriched, adult male accessory axillary lymph node Mus musculus cDNA clone G630076H03 5', mRNA sequence.				
ACCESSION	BY733751				
VERSION	BY733751.1 GI:27146878				
KEYWORDS	EST.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				

REFERENCE

AUTHORS

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 664)

Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,
Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,
Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K.,
Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,
Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y.,
Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,
Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,
Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
Rogers,J., Birney,E. and Hayashizaki,Y.

TITLE

Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs

JOURNAL

Nature 420, 563-573 (2002)

MEDLINE

22354683

PUBMED

12466851

COMMENT

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Fax: 81-45-503-9216

Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/

Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P.,
Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F.,
Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y.,
Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M.,
Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N.,
Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M.,
Takeda,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.

Direct Submission

Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.

10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

FEATURES Location/Qualifiers
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 accessory axillary lymph node"

ORIGIN

Alignment Scores:

Pred. No.:	1.28e-45	Length:	664
Score:	483.50	Matches:	92
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Best Local Similarity:	73.02%	Mismatches:	9
Query Match:	75.78%	Indels:	11
DB:	6	Gaps:	2

US-10-631-258-13 (1-118) x BY733751 (1-664)

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